

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 860 Seconds
(without alignments)
6955.045 Million cell updates/sec

Title: US-09-645-590-1
Perfect score: 138
Sequence: 1 accccatccgctgctctca.....actgacctcgccctgtccc 138

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	138	100.0	551	6	ARI76719	Sequence
2	138	100.0	551	6	AX138816	Sequence
3	138	100.0	551	6	AX139001	Sequence
4	138	100.0	551	6	AX139420	Sequence
5	138	100.0	551	6	AX337554	Sequence
6	138	100.0	551	6	AX463054	Sequence
7	138	100.0	551	6	BD015786	Compound
8	138	100.0	551	6	BD015859	Compound
9	138	100.0	551	6	BD103561	Variant p
10	138	100.0	551	9	HUMNPY	K01911 Human neuro
11	138	100.0	551	11	G18330	sWSS1475 Er
12	138	100.0	568	9	BC029497	Homo sapi
13	113.2	82.0	122	6	AR416737	Sequence
14	113.2	82.0	122	6	BD112290	EST and e
15	91	65.9	325	6	ARI76715	Sequence
16	91	65.9	325	6	BD103557	Variant p
17	91	65.9	325	9	HUMNPY01	M14295 Human neuro
18	91	65.9	185516	9	AC004485	Homo sapi
19	89.4	64.8	182634	9	AC142353	Pan trogl
20	89.4	64.8	230701	2	AC147298	Pan trogl
21	84.2	61.0	169	6	AX897763	Sequence
22	84.2	61.0	169	6	BD033296	Sequence
23	69.6	50.4	561	10	BC043012	Mus muscu
24	65.4	47.4	452	4	OAR417904	Ovis arie
25	63.2	45.8	511	10	RATNPYA	M20373 Rat neuro
26	63.2	45.8	539	10	RATNPY	M15880 Rat neuro
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28	63	45.7	483	6	AX305379	Sequence
29	62.8	45.5	417	9	HUMNPYA	M15789 Human neuro
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36	42.4	30.7	269	10	AF286198	Mus muscu
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38	42.4	30.7	483	10	AF273768	M15792 Rat neuro
39	42.4	30.7	2680	10	RATNPY01	AF392060 Rattus no
40	42.4	30.7	8102	10	AF392057	Rattus no
41	42.4	30.7	8103	10	AF392057	Rattus no
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ALIGNMENTS

RESULT 1	ARI76719	ARI76719	551 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	ARI76719	Sequence 5 from patent US 6312890.				
DEFINITION	ARI76719	Sequence 5 from patent US 6312890.				
ACCESSION	ARI76719	Sequence 5 from patent US 6312890.				
VERSION	ARI76719.1	GI:17919074				
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 551)				
TITLE		Koulu,M., Karvonen,M., Pesonen,U. and Uusitupa,M.				
		Diagnosis of a person's risk of developing atherosclerosis or				
		diabetic retinopathy based on leucine 7 to proline 7 polymorphism				
		in the prepro-neuropeptide Y gene				

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JOURNAL Patent: US 6312898-A 5 06-NOV-2001;
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QY 121 TGACCTCGCCCTGTCCC 138
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RESULT 2
AX138816 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097706.
ACCESSION AX138816
VERSION AX138816.1 GI:14274563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Phosphodiesterase inhibitors for the treatment of female sexual
JOURNAL Patent: EP 1097706-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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RESULT 3
AX139001 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097707.
ACCESSION AX139001
VERSION AX139001.1 GI:14274691
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Treatment of female sexual dysfunction
JOURNAL Patent: EP 1097707-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES Location/Qualifiers
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Db 121 TGACCTCGCCCTGTCCC 138

RESULT 4
AX139420 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Maw,G.N. and Wayman,C.P.
TITLE Nep inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
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AX337554
LOCUS AX337554 551 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 8063 from Patent WO0194629.
ACCESSION AX337554
VERSION AX337554.1 GI:18128273
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 8063 13-DEC-2001;
Avalon Pharmaceuticals (US)
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LOCUS AX463054 551 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 1 from Patent WO0247670.
ACCESSION AX463054
VERSION AX463054.1 GI:21886069
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Naylor, A.M., van der Graaf, P.H. and Wayman, C.P.
TITLE Treatment of male sexual dysfunction
JOURNAL Patent: WO 0247670-A 1 20-JUN-2002;
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BD015786
LOCUS BD015786 551 bp DNA linear PAT 27-AUG-2002
DEFINITION Compound for treatment of female sexual dysfunction.
ACCESSION BD015786
VERSION BD015786.1 GI:22556923
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Compound for treatment of female sexual dysfunction
JOURNAL Patent: JP 2001206855-A 4 31-JUL-2001;
PFIZER INC
COMMENT OS Homo sapiens (human)
PN JP 2001206855-A/4
PD 31-JUL-2001
PR 08-NOV-2000 JP 2000339905
PR 08-NOV-1999 GB 9926437.6, 18-FEB-2000 GB 0004021.2 PR
26-MAY-2000 GB 0013001.3, 05-JUL-2000 GB 0016563.9 PR
12-JUL-2000 GB 0017141.3
PI GRAHAM NIGEL MAW, CHRISTOPHER PETER WAYMAN
PC A61K45/00, A61K31/122, A61K31/165, A61K31/17, A61K31/18, A61K31/19,
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DEFINITION    Compound for treatment of female sexual dysfunction.
ACCESSION    BD015859
VERSION      BD015859.1 GI:22556996
KEYWORDS     JP 2001213802-A/4.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 551)
AUTHORS      Maw,G.N. and Wayman,C.P.
TITLE        Compound for treatment of female sexual dysfunction
JOURNAL      PFIZER INC
COMMENT      OS Homo sapiens (human)
              PN JP 2001213802-A/4
              PD 07-AUG-2001
              PR 08-NOV-2000 JP 2000339853
              PR 08-NOV-1999 GB 9926437.6,18-FEB-2000 GB 0004021.2 PR
              26-MAY-2000 GB 0013001.3,05-JUL-2000 GB 0016563.9 PR
              12-JUL-2000 GB 0017141.3
              PI GRAHAM NIGEL MAW,CHRISTOPHER PETER WAYMAN
              PC A61K45/00,A61K31/19,A61K31/192,A61K31/4015,A61K31/433,A61K31/
              PC 44,A61P15/00,
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LOCUS          551 bp      RNA      linear      PAT 27-AUG-2002
DEFINITION    Variant preproenkephalin Y, DNA molecule encoding variant signal
              peptide and utilization of the same.
ACCESSION    BD103561
VERSION      BD103561.1 GI:22649135
KEYWORDS     JP 2001526296-A/5.
SOURCE       unidentified
              unclassified.
              1 (bases 1 to 551)
REFERENCE
AUTHORS      Koulou,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
TITLE        Variant preproenkephalin Y, DNA molecule encoding variant signal
              peptide and utilization of the same
JOURNAL      HORMONES MEDICAL OY LTD
COMMENT      OS Unidentified
              PN JP 2001526296-A/5
              PD 18-DEC-2001
              PR 16-DEC-1998 JP 2000525455
              PR 19-DEC-1997 US 08/994946
              PI MARKKU KOULOU,MATTI KARVONEN,ULLAMARI PESONEN,MATTI UUSITUPA PC
              A61P43/00,
              PC C07K16/26,C12N15/10,C12N15/09,C12Q1/68,G01N33/15,G01N33/50// PC
              C12P21/08,
              PC A61K37/02,A61K37/24,C12N5/00,C12N15/00
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              CC Topology: Linear;
              CC Variant preproenkephalin Y, DNA molecule encoding variant
              CC signal peptide
              CC and utilization of the same
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HUMNPY
LOCUS          551 bp      mRNA      linear      PRI 07-JAN-1995
DEFINITION    Human neuropeptide Y (NPY) mRNA, complete cds.
ACCESSION    K01911
VERSION      K01911.1 GI:189273
KEYWORDS     neuropeptide Y.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 551)
REFERENCE
AUTHORS      Minth,C.D., Bloom,S.R., Polak,J.M. and Dixon,J.E.
TITLE        Cloning, characterization, and DNA sequence of a human cDNA
              encoding neuropeptide tyrosine
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 81 (14), 4577-4581 (1984)
MEDLINE      84272678
PUBMED       6589611
COMMENT      Original source text: Human pheochromocytoma, cDNA to mRNA, clone
              pNPY3-75.
              Neuropeptide Y (NPY) is one of the most abundant peptides in the
              mammalian nervous system, and its extensive distribution suggests a
              neuro-transmitter or -modulator role. NPY is also found in some
              chromaffin cells of the adrenal medulla.
              Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 4.6e-23;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 TGACCCCTCGCCCTGTCCC 138
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RESULT 11
G18330
LOCUS
DEFINITION SW51475 Eric D. Green Homo sapiens STS genomic, sequence tagged
site.
ACCESSION G18330
VERSION G18330.1 GI:1222787
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
Leckie,M.P. and Green,E.D.
TITLE A collection of 1814 human chromosome 7-specific STSs
JOURNAL Genome Res. 7 (1), 59-64 (1997)
MEDLINE 97189344
PUBMED 9037602
REFERENCE 2 (bases 1 to 551)
AUTHORS Green,E.D.
TITLE Human chromosome 7 STSs (1997)
JOURNAL Unpublished (1997)
COMMENT Synonyms: NPY
GDB: GDB:3754247
GDB_DSEG: NPY

```

Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CCACCCATCTTACCAATG
Primer B: GACAAAGGAACACATTGCAG
STS size: 60
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 55 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600

Protocol:
Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

This STS was developed from sequence determined by another investigator. See GenBank record: K01911 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].

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Best Local Similarity 100.0%; Pred. No. 4.6e-23;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCCCGTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
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Db 61 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCCCTCGCCCTGTCCC 138
Db 121 TGACCCCTCGCCCTGTCCC 138

RESULT 12
BC029497
LOCUS
DEFINITION Homo sapiens neuropeptide Y, mRNA (cdna clone MGC:33138
IMAGE:5278692), complete cds.

BC029497 568 bp mRNA linear PRI 06-OCT-2003
Homo sapiens neuropeptide Y, mRNA (cdna clone MGC:33138
IMAGE:5278692), complete cds.

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ACCESSION BC029497
VERSION BC029497.1 GI:20809582
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS Strausberg, R.D., Collins, F.S., Wagner, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,
Hopkins, R.F., Jordan, H., Moore, J., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McKean, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A.C., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnurch, A., Schein, J.E., Jones, S.J., Skalska, U., Smalhus, D.E.,
Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalhus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
PUBMED 2238257
MEDLINE 12477932
REFERENCE 2 (bases 1 to 568)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IPAK Plate: 48 Row: n Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505448.
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location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.6e-23;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGCTCGCCGACAGCATAGTACTTCCGCG 60
Db 3 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGCTCGCCGACAGCATAGTACTTCCGCG 62
QY 61 CCAGCCAGCCCGCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120
Db 63 CCAGCCAGCCCGCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 122
QY 121 TGACCTCGCTGCTGCTCC 138
Db 123 TGACCTCGCTGCTGCTCC 140
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LOCUS AR416737 122 bp DNA linear PAT 18-DRC-2003
DEFINITION Sequence 8234 from patent US 6639063.
ACCESSION AR416737
VERSION AR416737.1 GI:40171847
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 122)
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 8234 28-OCT-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 94.3%; Pred. No. 4.8e-17;
Matches 115; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Db 61 CCAGCCAGCCCGCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120
QY 121 TG 122
Db 121 TG 122
RESULT 14
BD112290
LOCUS BD112290 122 bp DNA linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD112290
VERSION BD112290.1 GI:23207108
KEYWORDS JP 2002010789-A/4367.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 122)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 4367 15-JAN-2002;
GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/4367
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
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Best Local Similarity 94.3%; Pred. No. 4.8e-17;
Matches 115; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60
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DB 1 ACCCCATCGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTGGCGC 60
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Search completed: April 26, 2004, 14:33:35
Job time : 862 secs
RESULT 15
AR176715
LOCUS 325 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6312898.
ACCESSION AR176715
VERSION AR176715.1 GI:17919070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 325)
AUTHORS Koulou,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
TITLE Diagnosis of a person's risk of developing atherosclerosis or
diabetic retinopathy based on leucine 7 to proline 7 polymorphism
in the prepro-neuropeptide Y gene
JOURNAL Patent: US 6312898-A 1 06-NOV-2001;
FEATURES
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Query Match 65.9%; Score 91; DB 6; Length 325;
Best Local Similarity 90.7%; Pred. No. 8.1e-12;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTG 107
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DB 270 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTGCTACGACCCGCTG 316
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
2155.336 Million cell updates/sec

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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Maximum Match 100%

Listing first 45 summaries

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5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	138	100.0	551	3	AAC60348 Human neu
5	138	100.0	551	4	AAD14527 Human neu
6	138	100.0	551	4	AAD14517 Human neu
7	138	100.0	551	4	AAD14517 Human neu
8	138	100.0	551	4	AAD14517 Human neu
9	138	100.0	551	6	ABL69726 Human neu
10	138	100.0	551	6	ABL69726 Human neu
11	138	100.0	551	6	ABL69726 Human neu
12	138	100.0	551	7	ACF63372 Human neu
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16	111	80.4	553	4	AAF72771 Human pro
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18	91	65.9	325	3	AAC60344 Human neu
19	91	65.9	325	6	AAL47340 Human neu
20	91	65.9	722	6	AAL47344 Human neu
21	91	65.9	14537	6	AAL48078 Human neu
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23	90.8	65.8	609	5	ABV44088 Human pro

24	89.4	64.8	496	8	ACH15527 Human adu
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27	87	63.0	562	5	ABV23158 Human pro
28	87	63.0	562	5	ABV28999 Human pro
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31	63.2	45.8	707	6	ABT09021 Phase-1 R
32	63	45.7	483	6	ABT09021 Mouse isc
33	63	45.7	1185	5	ABV29161 Human pro
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38	63	45.7	1185	5	ABV22776 Human pro
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ALIGNMENTS

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AC	AAL42206;
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DT	13-JUN-2002 (first entry)
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DE	Human neurotensin Y (NPY) mRNA sequence, binding structure 2.
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KW	Human; ss; stress-induced neurotensin Y overproduction; NPY;
KW	neurotransmitter; central nervous system; peripheral nervous system;
KW	heart rate reduction; insulin secretion enhancement; NPY mRNA;
KW	binding structure 2.
XX	
OS	Homo sapiens.
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FT	WO200215941-A1.
FT	
FT	28-FEB-2002.
FT	
FT	31-JUL-2001; 2001WO-FI000687.
FT	
FT	25-AUG-2000; 2000US-00645590.
FT	
FT	(HORM-) HORMOS MEDICAL CORP.

XX Koulou M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;
 PI WPI; 2002-269319/31.
 XX
 DR
 XX
 PT Reducing stress-induced overproduction of neuropeptide Y (NPY) in an
 PT individual useful for reducing heart rate and enhancing insulin
 XX secretion.
 PS Disclosure; Page 23; 45pp; English.
 XX
 CC The invention comprises a method for reducing stress-induced
 CC overproduction of neuropeptide Y (NPY) in an individual. NPY is the most
 CC abundant neuropeptide and an important neurotransmitter in the human
 CC central and peripheral nervous system. The method of the invention is
 CC useful for reducing constitutive overexpression of NPY in the endothelial
 CC cells of an individual, in order to reduce the heart rate and enhance
 CC insulin secretion. The method of the invention is also useful for
 CC diagnosing susceptibility to stress-induced overproduction of NPY. The
 CC present sequence represents binding structure 2 of the human NPY mRNA
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 SQ Sequence 138 BP; 23 A; 61 C; 34 G; 20 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 6; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.3e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCCGACAGCATAGTACTTGGCCG 60
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 Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCTCGCCCTGTCCC 138
 Db 121 TGACCTCGCCCTGTCCC 138
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 AC AAL42205;
 XX
 DT 13-JUN-2002 (first entry)
 XX
 DE Human neuropeptide Y (NPY) mRNA sequence, binding structure 1.
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 KW Human; ss; stress-induced neuropeptide Y overproduction; NPY;
 KW neurotransmitter; central nervous system; peripheral nervous system;
 KW heart rate reduction; insulin secretion enhancement; NPY mRNA;
 KW binding structure 1.
 XX
 OS Homo sapiens.
 XX
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 PN WO2002I5941-A1.
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 PD 28-FEB-2002.
 XX
 PF 31-JUL-2001; 2001WO-FI000687.
 XX
 PR 25-AUG-2000; 2000US-00645590.
 XX

(HORM-) HORMOS MEDICAL CORP.
 Koulou M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;
 WPI; 2002-269319/31.
 Reducing stress-induced overproduction of neuropeptide Y (NPY) in an
 individual useful for reducing heart rate and enhancing insulin
 secretion.
 Disclosure; Page 22; 45pp; English.
 The invention comprises a method for reducing stress-induced
 overproduction of neuropeptide Y (NPY) in an individual. NPY is the most
 abundant neuropeptide and an important neurotransmitter in the human
 central and peripheral nervous system. The method of the invention is
 useful for reducing constitutive overexpression of NPY in the endothelial
 cells of an individual, in order to reduce the heart rate and enhance
 insulin secretion. The method of the invention is also useful for
 diagnosing susceptibility to stress-induced overproduction of NPY. The
 present sequence represents binding structure 1 of the human NPY mRNA
 Sequence 138 BP; 23 A; 61 C; 34 G; 20 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 6; Length 138;
 Best Local Similarity 100.0%; Pred. No. 2.3e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCCGACAGCATAGTACTTGGCCG 60
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 Db 61 CCAGCCACGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCTCGCCCTGTCCC 138
 Db 121 TGACCTCGCCCTGTCCC 138
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 ID AAX86051 standard; cDNA; 551 BP.
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 AC AAX86051;
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 DT 14-SEP-1999 (first entry)
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 DE cDNA encoding human prepro-neuropeptide Y (NPY).
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 KW Human neuropeptide Y; NPY; prepro-neuropeptide Y; mutant;
 KW serum cholesterol; low density lipoprotein; LDL; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT sig_peptide 87..170
 FT /*tag= b
 FT mutation 106
 FT /*tag= c
 FT /note= "this base is changed to C to encode the mutant
 FT protein of the invention"
 FT
 PN WO9932518-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 16-DEC-1998; 98WO-FI000985.
 XX
 PR 19-DEC-1997; 97US-00994946.
 XX

XX (HORM-) HORMOS MEDICAL LTD OY.
 XX Koulou M, Karvonen M, Pesonen U, Uusitupa M;
 XX WPI; 1999-405161/34.
 DR P-PSDB; AAY23828.
 XX
 XX New polynucleotide (I) encoding a prepro-neuropeptide Y (preproNPY).
 XX Claim 2; Fig 1c; 45pp; English.
 XX
 XX The present sequence encodes human prepro-neuropeptide Y (NPY). The
 CC specification describes a polynucleotide encoding a prepro-neuropeptide Y
 CC (preproNPY), where leu (7) is substituted by pro(7). This polynucleotide
 CC is useful for diagnosing and treating humans with a predisposition for
 CC increased serum cholesterol or low density lipoprotein (LDL)
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 138; DB 2; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
 Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
 QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
 Db 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
 QY 121 TGACCCCTCGCCCTGTCCC 138
 Db 121 TGACCCCTCGCCCTGTCCC 138
 RESULT 4
 AAC60348
 ID AAC60348 standard; DNA; 551 BP.
 AC AAC60348;
 XX
 XX 16-FEB-2001 (first entry)
 DT Human neuropeptide Y coding DNA.
 DE NPY; neuropeptide Y; gene therapy; atherosclerosis; diabetic retinopathy;
 KW ds.
 KW Homo sapiens.
 OS WO200063430-A1.
 XX
 XX 26-OCT-2000.
 PD
 XX 29-MAR-2000; 2000WO-FI000260.
 PF
 XX 15-APR-1999; 99US-00291994.
 PR
 XX (HORM-) HORMOS MEDICAL LTD OY.
 PA Koulou M, Karvonen M, Pesonen U, Uusitupa M;
 PI WPI; 2000-679606/66.
 DR
 XX Diagnosing diabetic person's susceptibility for developing
 PT atherosclerosis or diabetic retinopathy involves detecting leucine7 to
 PT proline7 polymorphism in signal peptide part of human prepro neuropeptide
 PT Y.
 XX Disclosure; Fig 1; 4lpp; English.
 ES

CC The present invention relates to diagnosing a diabetic person's
 CC susceptibility for having an increased risk of developing atherosclerosis
 CC or diabetic retinopathy involves determining whether the subject has a
 CC substitution of leucine 7 for proline in the signal peptide part of human
 XX prepro-neuropeptide Y
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 3; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
 Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGC CGC 60
 QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
 Db 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAC 120
 QY 121 TGACCCCTCGCCCTGTCCC 138
 Db 121 TGACCCCTCGCCCTGTCCC 138
 RESULT 5
 AAD14527
 ID AAD14527 standard; DNA; 551 BP.
 XX
 AC AAD14527;
 XX
 XX 01-NOV-2001 (first entry)
 DT Human neuropeptide Y (NPY) DNA.
 DE Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
 KW FSAD; neutral endopeptidase inhibitor; I-NEP; enkephalinase;
 KW gynaecological; endopeptidase-2; neuropeptide Y; NPY; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 87..360
 FT /*tag= a
 FT /product= "Human NPY"
 FT sig_peptide 87..170
 FT /*tag= b
 FT mat_peptide 171..278
 FT /*tag= c
 FT /product= "Human mature NPY protein"
 XX
 XX EPI097719-A1.
 XX
 XX 09-MAY-2001.
 PD
 XX
 XX 03-NOV-2000; 2000EP-00309722.
 PF
 XX 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.
 PR 12-JUL-2000; 2000GB-00017141.
 XX
 XX (PFIZ) PFIZER LTD.
 XX (PFIZ) PFIZER INC.
 XX
 XX Maw GN, Wayman CP;
 XX WPI; 2001-309880/33.
 DR P-PSDB; AAE07955.
 XX
 XX Treating females suffering from female sexual dysfunction, preferably
 PT female sexual arousal dysfunction using a neutral endopeptidase inhibitor

PT that potentiates cAMP in female genitalia.
 PS Disclosure; Page 97; 124pp; English.
 XX
 CC The present invention relates to a method for treating female sexual
 CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).
 CC The method comprising using an agent, an inhibitor of neutral
 CC endopeptidase (NEP) EC 3.4.24.11 or I-NEP, which is capable of
 CC potentiating cAMP (which enhances female genital blood flow) in the
 CC sexual genitalia of the females. NEP is also known as enkephalinase or
 CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier
 CC or excipient. The method restores a normal sexual arousal response,
 CC particularly increased blood flow leading to vaginal, clitoral and labial
 CC engorgement. This will result in increased vaginal lubrication via plasma
 CC transduction, increased vaginal compliance and increased genital (e.g.
 CC vaginal and clitoral) sensitivity. The present sequence is human
 CC neuropeptide Y (NPY) DNA used in the method of the invention
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 4; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACACATAGTACTTGGCGC 60
 DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACACATAGTACTTGGCGC 60
 QY 61 CCAGCCAGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
 DB 61 CCAGCCAGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCCCTCGCCCTGTGCC 138
 DB 121 TGACCCCTCGCCCTGTGCC 138
 RESULT 6
 AAD14517
 ID AAD14517 standard; DNA; 551 BP.
 XX
 AC AAD14517;
 DT 01-NOV-2001 (first entry)
 XX Human neuropeptide Y (NPY) DNA.
 DE Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
 KW FSAD; neuropeptide Y; NPY; gynaecological; vasoactive intestinal peptide;
 KW VIP; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT sig_peptide /product= "Human NPY protein"
 FT 87..170
 FT /*tag= b
 FT mat_peptide 171..278
 FT /*tag= c
 FT /product= "Human mature NPY protein"
 XX
 EP1097718-A1.
 FN
 XX
 PD 09-MAY-2001.
 XX
 PF 03-NOV-2000; 2000EP-00309720.
 XX
 PR 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.

PR 12-JUL-2000; 2000GB-00017141.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Maw GN, Wayman CP;
 XX
 WIPI; 2001-319199/34.
 P-PSDB; AAE07919.
 XX
 PT Treating females suffering from female sexual dysfunction, preferably
 PT female sexual arousal dysfunction using a neuropeptide Y inhibitor that
 PT potentiates cAMP in female genitalia.
 XX
 PS Disclosure; Page 129; 165pp; English.
 XX
 CC The patent discloses a method for the treatment of a female suffering
 CC from female sexual dysfunction (FSD), preferably female sexual arousal
 CC dysfunction (FSAD) by the use of an agent which is an inhibitor of
 CC neuropeptide Y (NPY). The agent is capable of potentiating cAMP which
 CC enhances female genital (e.g. vaginal or clitoral) blood flow in the
 CC sexual genitalia of the female and is optionally admixed with a diluent
 CC carrier or excipient. The method restores a normal sexual arousal
 CC response namely, increased blood flow leading to vaginal, clitoral and
 CC labial engorgement. This will result in increased vaginal lubrication via
 CC plasma transduction, increased vaginal compliance and increased genital
 CC (e.g. vaginal and clitoral) sensitivity. The method is used for treating
 CC a female suffering from FSD preferably FSAD. The present sequence is a
 CC DNA encoding human neuropeptide Y (NPY) protein. NPY exerts an inhibitory
 CC influence over VIP-mediated vasorelaxation and NPY Y1 receptor
 CC antagonists will facilitate the vasoactive effect of endogenous
 CC vasoactive intestinal peptide (VIP) released during arousal and enhances
 CC vaginal engorgement
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 4; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACACATAGTACTTGGCGC 60
 DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACACATAGTACTTGGCGC 60
 QY 61 CCAGCCAGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
 DB 61 CCAGCCAGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCCCTCGCCCTGTGCC 138
 DB 121 TGACCCCTCGCCCTGTGCC 138
 RESULT 7
 AAF84086
 ID AAF84086 standard; DNA; 551 BP.
 XX
 AC AAF84086;
 DT 22-AUG-2001 (first entry)
 XX Human neuropeptide Y (NPY) encoding DNA.
 DE Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
 KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;
 KW cGMP; medicament; human; neuropeptide Y; NPY; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT /product= "neuropeptide Y"

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FT sig_peptide /gene= "NPY"
FT 87..170 /*tag= b
FT 171..377 /*tag= c
FT mat_peptide
FT
PN EPI097706-A1.
XX
XX 09-MAY-2001.
XX
XX 03-NOV-2000; 2000EP-00309719.
XX
XX 08-NOV-1999; 99GB-00026437.
XX 18-FEB-2000; 2000GB-00004021.
XX 26-MAY-2000; 2000GB-00013001.
XX 05-JUL-2000; 2000GB-00016563.
XX 12-JUL-2000; 2000GB-00017141.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Maw GN, Wayman CP;
XX
XX WPI; 2001-383217/41.
XX P-PSDB; AAB85118.
XX
XX Novel pharmaceutical composition for treating female sexual dysfunction,
XX preferably female sexual arousal disorder, comprising an agent capable of
XX potentiating cAMP in the sexual genitalia of the female.
XX
XX Disclosure; Page 104; 135pp; English.
XX
XX The invention provides a pharmaceutical composition for treating female
XX sexual dysfunction (FSD), preferably female sexual arousal disorder
XX (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
XX in a female. The composition comprises an agent capable of potentiating
XX cAMP in the sexual genitalia of the female. The agent is an inhibitor
XX (1:PDE) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally
XX cGMP). The agent is useful in the manufacture of a medicament for the
XX treatment of FSD, preferably FSAD, by potentiating cAMP in the sexual
XX genitalia. It is also useful in the manufacture of a medicament for
XX enhancing female genital (e.g., vaginal or clitoral) blood flow. The
XX present sequence represents a human neuropeptide Y (NPY) encoding DNA
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 138; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
DB 1 ACCCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTACAGCGACTGGGCTGTCCGGAC 120
DB 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCCCTGGCCCTGTCCC 138
DB 121 TGACCCCTGGCCCTGTCCC 138
RESULT 8
ID AAF84076
XX AAF84076 standard; DNA; 551 BP.
XX AAF84076;
XX
XX 22-AUG-2001 (first entry)
XX
XX Human neuropeptide Y (NPY) encoding DNA.
XX

```

```

KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;
XX cGMP; medicament; human; neuropeptide Y; NPY; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 87..380
XX /*tag= a
XX /product= "neuropeptide Y"
XX /gene= "NPY"
XX sig_peptide 87..170
XX /*tag= b
XX mat_peptide 171..377
XX /*tag= c
XX
XX EPI097706-A1.
XX
XX 09-MAY-2001.
XX
XX 03-NOV-2000; 2000EP-00309718.
XX
XX 08-NOV-1999; 99GB-00026437.
XX 18-FEB-2000; 2000GB-00004021.
XX 26-MAY-2000; 2000GB-00013001.
XX 05-JUL-2000; 2000GB-00016563.
XX 12-JUL-2000; 2000GB-00017141.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Maw GN, Wayman CP;
XX
XX WPI; 2001-383216/41.
XX P-PSDB; AAB85107.
XX
XX Novel pharmaceutical composition for treating female sexual dysfunction,
XX preferably female sexual arousal disorder, comprising an agent capable of
XX potentiating cAMP in the sexual genitalia of the female.
XX
XX Disclosure; Page 102; 132pp; English.
XX
XX The invention provides a pharmaceutical composition for treating female
XX sexual dysfunction (FSD), preferably female sexual arousal disorder
XX (FSAD), or enhancing female genital (e.g. vaginal or clitoral) blood flow
XX in a female. The composition comprises an agent capable of potentiating
XX cAMP in the sexual genitalia of the female. The agent is an inhibitor
XX (1:PDE) of phosphodiesterase (PDE), which hydrolyzes cAMP (optionally
XX cGMP). The agent is useful in the manufacture of a medicament for the
XX treatment of FSD, preferably FSAD, by potentiating cAMP in the sexual
XX genitalia. It is also useful in the manufacture of a medicament for
XX enhancing female genital (e.g., vaginal or clitoral) blood flow. The
XX present sequence represents a human neuropeptide Y (NPY) encoding DNA
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 138; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
DB 1 ACCCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTACAGCGACTGGGCTGTCCGGAC 120
DB 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCCCTGGCCCTGTCCC 138
DB 121 TGACCCCTGGCCCTGTCCC 138

```

RESULT 9
 ID ABL69726 standard; DNA; 551 BP.
 XX AC ABL69726;
 XX DT 15-MAY-2002 (first entry)
 XX DE Prostate cancer related gene sequence SEQ ID NO:8063.
 XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX OS Homo sapiens.
 XX FN WO200194629-A2.
 XX PD 13-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US010838.
 XX PR 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 26-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX (AVAL-) AVALON PHARM.
 XX PA Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-198264/24.
 XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX PS Claim 1; SEQ ID NO 8063; 44pp; English.
 XX CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 100.0%; Score 138; DB 6; Length 551;
 Best Local Similarity 100.0%; Pred. No. 2.6e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCTGC 60
 Db 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGCCTGC 60
 QY 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGAC 120
 Db 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGAC 120
 QY 121 TGACCTCGCCCTGTCTCC 138
 Db 121 TGACCTCGCCCTGTCTCC 138
 RESULT 10
 ABL69726
 ID ABL69726 standard; cDNA; 551 BP.
 XX AC ABL69726;
 XX DT 23-SEP-2002 (first entry)
 XX DE Human neuropeptide Y nucleotide sequence.
 XX KW Neuropeptide Y; NPY; human; inhibitor; male sexual dysfunction;
 KW male erectile dysfunction; obesity; anorexia; bulimia; vasotropic;
 KW anorectic; therapy; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200247670-A1.
 XX PD 20-JUN-2002.
 XX PF 10-DEC-2001; 2001WO-IB002399.
 XX PR 15-DEC-2000; 2000GB-00030647.
 PR 06-APR-2001; 2001GB-00008730.
 PR 23-APR-2001; 2001GB-00009910.
 PR 04-MAY-2001; 2001GB-00011037.
 PR 29-JUN-2001; 2001US-00895367.
 PR 13-JUL-2001; 2001US-00905846.
 PR 24-AUG-2001; 2001GB-00020679.
 XX

PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
XX
XX PI Naylor AM, Van Der Graaf PH, Wayman CP;
XX
XX DR WPI; 2002-547828/58.
XX
XX PT Use of an inhibitor of neuropeptide Y in the preparation of medicament
PT for the treatment or prevention of male erectile dysfunction.
XX
XX PS Disclosure; Fig 4; 179pp; English.
XX
XX CC The present sequence is a human neuropeptide Y (NPY) polynucleotide
CC sequence. The invention relates to the use of an inhibitor of NPY, or an
CC inhibitor of an NPY Y1 receptor, especially an inhibitor selective for an
CC NPY or NPY Y1 receptor associated with male genitalia, in the preparation
CC of a medicament for the treatment or prevention of male sexual
CC dysfunction, especially male erectile dysfunction (MED). A polypeptide
CC encoded by the present sequence may be used as a target in screens to
CC identify agents capable of inhibiting NPY. NPY may also be used as a
CC target to identify agents capable of mediating an increase in
CC intracavernosal pressure through the inhibition of NPY. The inhibitor
CC selectively increases intracavernosal pressure of the penis which
CC facilitates and/or causes penile erection during sexual arousal. In
CC addition to treatment of MED, the inhibitor can also be used to treat
CC abnormal drink and food intake disorders, such as obesity, bulimia,
CC anorexia and metabolic disorders (all claimed)
XX
SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 138; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60

QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGGAC 120

QY 121 TGACCCCTGGCCCTGTCCC 138
Db 121 TGACCCCTGGCCCTGTCCC 138

RESULT 11
AAL47339
ID AAL47339 standard; cDNA; 551 BP.
XX
XX AC AAL47339;
XX
XX DT 18-SEP-2002 (first entry)
XX
XX DE Human neuropeptide Y coding sequence.
XX
XX KW Human; neuropeptide Y; NPY; chromosome 7q15.1; SNP; obesity; BMI;
KW body mass index; single nucleotide polymorphism; gene; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 87..380
FT /*tag= a
FT /*product= "NPY"
FT sig_peptide 87..170
FT /*tag= b
FT variation replace(106,C)
FT /*tag= d
FT mat_peptide 171..380
FT /*tag= c
XX

PN WO200236825-A1.
XX
XX PD 10-MAY-2002.
XX
XX PF 02-NOV-2001; 2001WO-SE002431.
XX
XX PR 03-NOV-2000; 2000SE-00004035.
XX
XX PA (PHAA) PHARMACIA AB.
XX
XX PI Wahlestedt C, Ding B;
XX
XX DR WPI; 2002-500129/53.
XX
XX DR P-PSDE; AAO18054.
XX
XX PT Diagnosing single nucleotide polymorphism(s) in the human neuropeptide Y
PT (NPY) gene, useful for diagnosing a predisposition to e.g. obesity, by
PT determining the nucleic acid sequence at one or more positions of the NPY
PT gene in the human.
XX
XX PS Example 5; Page 28-29; 37pp; English.
XX
XX CC The present invention relates to a method of diagnosing a predisposition
CC to obesity in humans by identifying a single nucleotide polymorphism
CC (SNP) at position 1128 (position 106 of this sequence) of the
CC neuropeptide Y gene. The gene is found at chromosome 7q15.1. The present
CC sequence is the NPY coding sequence
XX
SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 138; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCCATCCGCTGGCTCTCACCCCTCGGACGCTCGCCGACGATAGTACTTGGCGC 60

QY 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACGACCATGCTAGGTAAACAGCGACTGGGCTGTCCGGAC 120

QY 121 TGACCCCTGGCCCTGTCCC 138
Db 121 TGACCCCTGGCCCTGTCCC 138

RESULT 12
ACF63372
ID ACF63372 standard; DNA; 551 BP.
XX
XX AC ACF63372;
XX
XX DT 09-OCT-2003 (first entry)
XX
XX DE Human neuropeptide Y gene SEQ ID NO:94.
XX
XX KW Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;
KW dermatological; antidepressant; tranquilliser; antiinflammatory; eczema;
KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;
KW gynaecological; virucide; vulnary; antiarthritic; antiporiatic; cold;
KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
KW constipation; headache; seizure; multiple sclerosis; polymyositis;
KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
KW skin disorder; gene; ds.
XX
XX OS Homo sapiens.

```
XX WO2003006478-A1.
XX
XX 23-JAN-2003.
XX
XX 10-JUL-2002; 2002WO-US021664.
XX
XX 10-JUL-2001; 2001US-0303820P.
XX
XX (Olig-) OLIGOS ETC INC.
XX
XX Dale RMK, Arrow A, Thompson T;
XX
XX WPI; 2003-221709/21.
XX
XX Composition with a modified oligonucleotide useful for treating a patient
XX with a pathological disorder such as abnormal appetite, hypertension,
XX eczema, anxiety, stress, and cancer.
XX
XX Claim 6; Page 97; 173pp; English.
XX
XX The present invention describes a composition (I) suitable for
XX administration in a mammal, which comprises a modified oligonucleotide
XX (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
XX linked by achiral 5'-3' internucleoside phosphate linkages, where the
XX modified oligonucleotide is complementary to a region of a gene
XX associated with a pathological disorder. Also described: (1) a
XX nutritional supplement comprising (II); and (2) a cosmetic composition
XX comprising (II), where the modified oligonucleotide is complementary to a
XX region of a gene associated with a skin disorder. (I) and (II) can have
XX hypotensive, antihypertensive, vasotropic, dermatological, antidepressant,
XX tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,
XX neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
XX vulnerary, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
XX litholytic activities. (I) can be used for treating a patient with a
XX pathological disorder selected from abnormal appetite, hypertension,
XX hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
XX depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
XX colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
XX migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
XX fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
XX chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
XX chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
XX inflammation, heart burn, infection, poison ivy, colon cancer, malignant
XX melanoma, and malignant nasal polyps. The nutritional supplement is
XX useful for supplementing the diet of an individual, and the cosmetic
XX composition is useful for improving the appearance of the skin in an
XX individual with a skin disorder. ACP63279 to ACP63410 represent
XX nucleotide sequence given in the exemplification of the present invention
XX
XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 138; DB 7; Length 551;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-30;
XX Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
XX
XX 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
XX
XX 61 CCAGCCACGCCCGCGCGGCGAGCCACATGCTAGGTAGTAACAGCGACTGGGGCTGTCGGGAC 120
XX
XX 61 CCAGCCACGCCCGCGCGGCGAGCCACATGCTAGGTAGTAACAGCGACTGGGGCTGTCGGGAC 120
XX
XX 121 TCACCTCGCCCTGTCCC 138
XX
XX 121 TCACCTCGCCCTGTCCC 138
XX
XX RESULT 13
XX AAF72746
XX ID AAF72746 standard; cDNA; 969 BP.
XX
XX
XX AC AAF72746;
XX
XX 24-APR-2001 (first entry)
XX
XX Human prostate cancer antigen coding sequence #6.
XX
XX Immunosuppressive; neutrotropic; neuroprotective; antiviral; vulnerary;
XX anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
XX immune disorder; cardiovascular disorder; neurological disease;
XX infection; cancer; cytostatic; antiarthritic; antirheumatic;
XX antiasthmatic; anticonvulsant; vasotropic; vulnerary; human;
XX secreted protein; prostate cancer antigen; ss.
XX
XX Homo sapiens.
XX
XX WO200107476-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019666.
XX
XX 21-JUL-1999; 99US-0144972P.
XX
XX 13-AUG-1999; 99US-0148681P.
XX
XX 17-AUG-1999; 99US-0149173P.
XX
XX 06-OCT-1999; 99US-0158004P.
XX
XX 05-APR-2000; 2000US-0194689P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Birse C;
XX
XX WPI; 2001-138554/14.
XX
XX P-PSDB; AAB80278.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
XX antigens, useful for the diagnosis and treatment of disorders such as
XX cancer, leukemia and autoimmune disease.
XX
XX Claim 1; Page 359-360; 433pp; English.
XX
XX The present invention relates to human secreted prostate cancer antigen
XX coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
XX The coding sequences and proteins of the present invention are useful for
XX preventing, treating or ameliorating a medical condition; and for the
XX diagnosis and treatment of diseases and disorders. Diseases and disorders
XX that can be diagnosed and treated include (auto)immune diseases (e.g.
XX graft versus host disease and rheumatoid arthritis), inflammatory and
XX allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
XX cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
XX arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
XX disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
XX retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
XX neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
XX and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
XX viruses or parasites. They may also be useful for wound healing,
XX epithelial cell proliferation, supporting cell culture, tissue
XX regeneration, birth control and as a food additive or preservative. The
XX coding sequences can be used to generate fusion proteins by linking the
XX coding sequences to the human immunoglobulin G FC portion coding sequence
XX (AAF72732) for increasing the stability of the fusion protein as compared
XX to the human protein only
XX
XX Sequence 969 BP; 246 A; 275 C; 225 G; 210 T; 0 U; 13 Other;
XX
XX Query Match 90.4%; Score 124.8; DB 4; Length 969;
XX Best Local Similarity 96.9%; Pred. No. 1.7e-26;
XX Matches 126; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 9 CGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCGCCAC 68
XX
XX 250 CGAGNNCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCGCCAC 309
XX
```


QY 69 GCCCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGACCCCTC 128
|||||
Db 310 GCCCGCGCCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGACCCCTC 369
|||||
QY 129 GCCCTGTCTCC 138
|||||
Db 370 GCCCTGTCTCC 379
|||||
RESULT 14
AAAF72771
ID AAF72771 standard; cDNA; 553 BP.
XX
AC AAF72771;
XX
DT 24-APR-2001 (first entry)
XX
DE Human prostate cancer antigen coding sequence #31.
XX
KW Immunosuppressive; nontropic; neuroprotective; antiviral; vulnary;
KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
KW immune disorder; cardiovascular disorder; neurological disease;
KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
KW antiasthmatic; anticonvulsant; vasotropic; vulnary; human;
KW secreted protein; prostate cancer antigen; ss.
XX
OS Homo sapiens.
XX
PN WO200107476-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019666.
XX
PR 21-JUL-1999; 99US-0144972P.
PR 13-AUG-1999; 99US-0148681P.
PR 17-AUG-1999; 99US-0149173P.
PR 06-OCT-1999; 99US-0158004P.
PR 05-APR-2000; 2000US-0194689P.
XX
(HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Birse C;
XX
XX WPI; 2001-138554/14.
DR P-PSDB; AAB80303.
XX
PT New nucleic acid molecule encoding human secreted prostate cancer
PT antigens, useful for the diagnosis and treatment of disorders such as
PT cancer, leukemia and autoimmune disease.
XX
XX Claim 1; Page 375; 433pp; English.
XX
CC The present invention relates to human secreted prostate cancer antigen
CC coding sequences (AAAF72741-AAAF72789) and proteins (AAB80273-AAB80321).
CC The coding sequences and proteins of the present invention are useful for
CC preventing, treating or ameliorating a medical condition; and for the
CC diagnosis and treatment of diseases and disorders. Diseases and disorders
CC that can be diagnosed and treated include (auto)immune diseases (e.g.
CC graft versus host disease and rheumatoid arthritis), inflammatory and
CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
CC and Creutzfeldt-Jakob disease) and infections caused by bacteria, fungi,
CC viruses or parasites. They may also be useful for wound healing,
CC epithelial cell proliferation, supporting cell culture, tissue
CC regeneration, birth control and as a food additive or preservative. The
CC coding sequences can be used to generate fusion proteins by linking the
CC coding sequences to the human immunoglobulin G FC portion coding sequence

CC (AAAF72732) for increasing the stability of the fusion protein as compared
CC to the human protein only
XX
SQ Sequence 553 BP; 148 A; 161 C; 125 G; 119 T; 0 U; 0 Other;
Query Match 80.4%; Score 111; DB 4; Length 553;
Best Local Similarity 99.2%; Pred. No. 1.5e-22;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 16 TCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCCGCG 75
|||||
Db 1 TCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCCGCG 60
|||||
QY 76 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGACCCCTGCCCTGT 135
|||||
Db 61 CGCAGCCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGACTGA-CCTGCCCTGT 119
|||||
QY 136 CCC 138
|||||
Db 120 CCC 122
|||||
RESULT 15
AAAF15665
ID AAF15665 standard; cDNA; 599 BP.
XX
AC AAF15665;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:100.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
(HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
DR P-PSDB; AAB56462.
XX
PT Prostate cancer associated gene sequences, referred to as prostate cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as prostate cancer.
XX
XX Claim 1; Page 679-680; 2338pp; English.
XX
CC AAF15566 to AAF15505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 599 BP; 163 A; 169 C; 139 G; 120 T; 0 U; 8 Other;

Query Match 80.4%; Score 111; DB 3; Length 599;
 Best Local Similarity 99.2%; Pred. No. 1.5e-22;
 Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 14 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCCCGACGACGCGCG 73

Qy 76 CGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTGT 135

Db 74 CGCCA-CCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTGT 132

Qy 136 CCC 138

Db 133 CCC 135

Search completed: April 26, 2004, 14:04:43
 Job time : 276 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 2161 seconds
(without alignments)
1906.979 Million cell updates/sec

Title: US-09-645-590-1

Perfect score: 138

Sequence: 1 accccatcgctgctctca.....actgacctcgccctgtccc 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_esti.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pbg.*

27: em_gss_vrl.*

28: gb_gssi.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	463	14	CA772698 i083g01.y
2	138	100.0	584	12	BI457963 603198956
3	138	100.0	873	13	BU930481 AGENCOURT
4	137	99.3	300	9	AU100303 AU100303

5	135	97.8	136	9	AU077324
6	128	92.8	521	9	AI879081
7	127	92.0	556	13	B0721485
8	127	92.0	557	13	BQ25183
9	127	92.0	963	13	BQ876913
10	126.4	91.6	550	9	AI928896
11	125.4	90.9	544	9	AI826374
12	125	90.6	468	13	BI101548
13	124	89.9	433	9	AI929147
14	114	82.6	567	13	BQ932266
15	106.8	77.4	1123	13	BQ86097
16	87	63.0	766	13	BQ930120
17	86.6	62.8	1695	10	BF680552
18	80	58.0	498	9	AI199681
19	71	51.4	424	9	AA061961
20	71	51.4	443	9	AI385504
21	71	51.4	492	13	BX527459
22	71	51.4	556	11	AK002982
23	71	51.4	585	13	BU937569
24	71	51.4	591	13	BU558492
25	71	51.4	600	13	BU604192
26	71	51.4	926	13	BU936355
27	69.6	50.4	489	10	BE653651
28	69.6	50.4	493	13	BQ84972
29	69.6	50.4	534	13	BQ084688
30	69.6	50.4	569	13	BQ564644
31	68.4	49.6	574	9	AI198311
32	66.2	48.0	435	14	CB792893
33	63.2	45.8	402	14	CB769232
34	63.2	45.8	520	12	BQ64369
35	63.2	45.8	529	14	CB719328
36	63.2	45.8	544	14	CB612099
37	63.2	45.8	587	14	CB585333
38	63	45.7	408	9	AA270394
39	63	45.7	483	14	W70782
40	62.2	45.1	570	12	BQ44605
41	61.6	44.6	364	13	BQ290146
42	56.6	41.0	454	14	CB741987
43	56.6	41.0	461	14	CB736748
44	56.6	41.0	499	14	CB712314
45	56.6	41.0	500	14	CB712006

ALIGNMENTS

RESULT 1

CA772698

LOCUS

DEFINITION

CA772698 463 bp mRNA linear EST 03-DEC-2002

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similar to SW:NEUY_HUMAN P01303 NEUROPEPTIDE Y PRECURSOR ;, mRNA

sequence.

CA772698

VERSION

CA772698.1 GI:26009965

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 463)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemshka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: i083g01.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 598
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source
1. 463
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NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

Query Match 100.0%; Score 138; DB 14; Length 463;
Best Local Similarity 100.0%; Pred. No. 2e-24; 0; Indels 0; Gaps 0;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 120
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QY 121 TGACCTCGCCCTGTCCC 138
Db 148 TGACCTCGCCCTGTCCC 165
RESULT 2
BI457963
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 584)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM11703 row: 0 column: 13
High quality sequence stop: 584.
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1. 584
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insert size 2.3 kb and normalized to RQ1 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

Query Match 100.0%; Score 138; DB 12; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 68 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 127
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Db 128 TGACCTCGCCCTGTCCC 145
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BU930481
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 873)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2942 row: 1 column: 16
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FEATURES
source
1. 873
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"

MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 598
Seq primer: -40RP from Gibco.
FEATURES
source
1. 463
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:613056"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

Query Match 100.0%; Score 138; DB 14; Length 463;
Best Local Similarity 100.0%; Pred. No. 2e-24; 0; Indels 0; Gaps 0;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGC 60
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Db 28 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGC 87
QY 61 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 120
Db 88 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 147
QY 121 TGACCTCGCCCTGTCCC 138
Db 148 TGACCTCGCCCTGTCCC 165
RESULT 2
BI457963
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 584)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM11703 row: 0 column: 13
High quality sequence stop: 584.
FEATURES
source
1. 584
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5278692"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to RQ1 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

Query Match 100.0%; Score 138; DB 12; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGC 60
|||||
Db 8 ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGC 67
QY 61 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 120
Db 68 CCAGCCAGCCGCGCGGCGGAGCAGCAGCATAGTACTAGTAAACAGGACTGGGGCTGTCGGGAC 127
QY 121 TGACCTCGCCCTGTCCC 138
Db 128 TGACCTCGCCCTGTCCC 145
RESULT 3
BU930481
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 873)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2942 row: 1 column: 16
High quality sequence stop: 510.
FEATURES
source
1. 873
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```

/clone="IMAGE:6668512"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: Sfii (ggccctcggcc); Site 2: Sfii
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGGC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGCACATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
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ORIGIN

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Query Match      100.0%; Score 138; DB 13; Length 873;
Best Local Similarity 100.0%; Pred. No. 2.4e-24;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 4 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 63
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGAC 120
Db 64 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGAC 123
QY 121 TGACCCCTCGCCCTGTCTCC 138
Db 124 TGACCCCTCGCCCTGTCTCC 141
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RESULT 4

```

AUI00303
LOCUS          300 bp mRNA linear EST 05-APR-2001
DEFINITION    Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
Zrv6c665 similar to Human neurotrophin Y (NPY) mRNA, mRNA sequence.
ACCESSION     AUI00303
VERSION       AUI00303.1 GI:13551432
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J.,
AUTHORS       Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S.,
Okubo,K., Suyama,A. and Sugano S.
In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
```

TITLE

JOURNAL

COMMENT

FEATURES

source

```

1..136
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Zrv6c665"
/clone_lib="Sugano cDNA library"
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ORIGIN

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Query Match      97.8%; Score 135; DB 9; Length 136;
Best Local Similarity 99.3%; Pred. No. 8.1e-24;
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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FEATURES

source

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1..300
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Zrv6c665"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match      99.3%; Score 137; DB 9; Length 300;
Best Local Similarity 99.3%; Pred. No. 3.2e-24;
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Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTCCCGC 60
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAACAGCGACTGGGGCTGTCCGGAC 120
QY 121 TGACCCCTCGCCCTGTCTCC 138
Db 121 TGACCCCTCGCCCTGTCTCC 138
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RESULT 5

```

AUI077324
LOCUS          136 bp mRNA linear EST 04-MAY-2000
DEFINITION    Sugano cDNA library Homo sapiens cDNA clone Zrv6c665
similar to 5'-end region of Human neurotrophin Y (NPY) mRNA, mRNA
sequence.
ACCESSION     AUI077324
VERSION       AUI077324.1 GI:7440000
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H.,
AUTHORS       Tsunoda,T., Watanabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A.
and Sugano,S.
Statistical analysis of the 5' untranslated region of human mRNA
using 'Oligo-Capped' cDNA libraries
Genomics 64 (3), 286-297 (2000)
20211373
10756096
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
This clone was obtained from a '5'-end-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
```

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

```

10756096
```

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Contact: Yutaka Suzuki
```

```

Department of Virology
```

```

Institute of Medical Science, University of Tokyo
```

```

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
```

```

Email: ysuzuki@ims.u-tokyo.ac.jp
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Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
```

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Sugano,S. Construction and characterization of a full
```

```

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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```

149-156 (1997)
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```

This clone was obtained from a '5'-end-enriched' cDNA library
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constructed by 'Oligo-Capping' method. The coding region starts
```

```

from the 50 bp upstream to the 3'-end.
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Location/Qualifiers
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1..136
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/clone_lib="Sugano cDNA library"
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Location/Qualifiers
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1..136
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/clone="Zrv6c665"
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/clone_lib="Sugano cDNA library"
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Location/Qualifiers
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1..136
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/clone="Zrv6c665"
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/clone_lib="Sugano cDNA library"
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Location/Qualifiers
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1..136
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/organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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/clone="Zrv6c665"
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/clone_lib="Sugano cDNA library"
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```

RESULT 6
LOCUS      AI879081          521 bp      mRNA      linear      EST 23-AUG-1999
DEFINITION au54b11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2518557 5' similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN); , mRNA sequence.
ACCESSION  AI879081
VERSION     AI879081.1      GI:5553130
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 521)
AUTHORS   Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisels,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
            WashU-NCI human EST Project
            Unpublished (1997)
            Other ESTs: au54b11.x1
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 425.
FEATURES   Location/Qualifiers
            1..521
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2518557"
             /sex="male"
             /tissue_type="frontal lobe"
             /dev_stage="5 months post-conception"
             /lab_host="DH10B"
             /clone_lib="Schneider fetal brain 00004"
             /note="Organ: brain; Vector: pBluescript SK (Stratagene);
            Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
            prepared from human fetal brain tissue. 5' and 3'
            adaptors were used in cloning as follows: 5' adaptor
            sequence:
            5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAATTAATATCCCCCCCCCCC-3'
            and 3' adaptor sequence:
            5'-GAGAGAGAGACTCGAGTTTCTTTTCTTTTCTTTT-3'. The library was
            size-selected for >0.5 kb inserts and has an average
            insert size estimated at 1.2 kb. This library was
            constructed using the CAP-trapper method for full-length
            enrichment and has not undergone amplification. Library
            was constructed by Dr. Claudio Schneider (LNCIB-Area
            Science Park, Trieste, Italy)."
ORIGIN
Query Match      92.8%; Score 128; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 6.5e-22;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11  CTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGC 70
          |||||
Db      1  CTGGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGC 60
          |||||

Qy      71  CCGCGCGCCAGCCACCATGCTAGGTAACAACGAGCTGGGGCTGTCCGACTGACCCCTGC 130
          |||||
Db      61  CCGCGCGCCAGCCACCATGCTAGGTAACAACGAGCTGGGGCTGTCCGACTGACCCCTGC 120
          |||||

Qy      131  CCTGTCCC 138
          |||||

```

```

Db      121  CCTGTCCC 128
          |||||

RESULT 7
LOCUS      BQ721485          556 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION AGENCOURT 8234409 Lupski sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6188546 5', mRNA sequence.
ACCESSION  BQ721485
VERSION     BQ721485.1      GI:21860382
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 556)
AUTHORS   NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbe-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM3584 row: f column: 03
            High quality sequence stop: 555.
FEATURES   Location/Qualifiers
            1..556
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:6188546"
             /sex="male"
             /tissue_type="sympathetic trunk"
             /dev_stage="adult, 16 yr"
             /lab_host="DH10B"
             /clone_lib="Lupski sympathetic trunk"
             /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
            NotI; Site 2: SalI; cDNA made by oligo-dr priming.
            Directionally cloned using the following adaptors:
            5'-TCGACCCAGCGGTCCG-3' and
            5'-GACTAGTCTAGTCGCGCGCGCCT(15)-3'. Size selected >
            1 kb for average insert length 1.9 kb. This is a primary
            library, non-amplified. Library constructed by Life
            Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
            College of Medicine); available through Life
            Technologies."
ORIGIN
Query Match      92.0%; Score 127; DB 13; Length 556;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  TGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCC 71
          |||||
Db      1  TGGCTCTCACCCCTCGGAGCGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCC 60
          |||||

Qy      72  CGCGCGCCAGCCACCATGCTAGGTAACAACGAGCTGGGGCTGTCCGACTGACCCCTGCC 131
          |||||
Db      61  CGCGCGCCAGCCACCATGCTAGGTAACAACGAGCTGGGGCTGTCCGACTGACCCCTGCC 120
          |||||

Qy      132  CTGTCCC 138
          |||||
Db      121  CTGTCCC 127
          |||||

RESULT 8
BQ925183

```

```

LOCUS      B0925183                557 bp    mRNA    linear    EST 20-AUG-2002
DEFINITION AGENCOURT 8821446 Lupski_sciatic nerve Homo sapiens cDNA clone
IMAGE:6203754 5', mRNA sequence.
ACCESSION  B0925183
VERSION     B0925183.1 GI:22340214
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 557)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13623 row: o column: 19
            High quality sequence stop: 556.
            Location/Qualifiers
                location=1..557
                organism="Homo sapiens"
                mol_type="mRNA"
                db_xref="taxon:9606"
                clone="IMAGE:6203754"
                sex="male"
                tissue_type="sciatic nerve"
                dev_stage="adult, 70 yr"
                lab_host="DH10B"
                clone_lib="Lupski sciatic nerve"
                notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                NotI; Site 2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:
                5'-TCGACCCACCGCTCCG-3' and
                5'-GACTAGTTCTAGATCGGAGCGGCGCCCT(15)-3'. Size selected >
                1 kb for average insert length 1.87 kb. This is a primary
                library, non-amplified. Library constructed by Life
                Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                College of Medicine) and is available through Life
                Technologies."

ORIGIN
Query Match      92.0%; Score 127; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 71
Db 1 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 60

QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 131
Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 120

QY 132 CTGTCCC 138
Db 121 CTGTCCC 127

RESULT 9
LOCUS      B0876913                963 bp    mRNA    linear    EST 16-AUG-2002
DEFINITION AGENCOURT 8417678 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6193004 5', mRNA sequence.
ACCESSION  B0876913
VERSION     B0876913.1 GI:22268921
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 963)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13595 row: o column: 21
            High quality sequence stop: 517.
            Location/Qualifiers
                location=1..963
                organism="Homo sapiens"
                mol_type="mRNA"
                db_xref="taxon:9606"
                clone="IMAGE:6193004"
                sex="male"
                tissue_type="sympathetic trunk"
                dev_stage="adult, 16 yr"
                lab_host="DH10B"
                clone_lib="Lupski sympathetic trunk"
                notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                NotI; Site 2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:
                5'-TCGACCCACCGCTCCG-3' and
                5'-GACTAGTTCTAGATCGGAGCGGCGCCCT(15)-3'. Size selected >
                1 kb for average insert length 1.9 kb. This is a primary
                library, non-amplified. Library constructed by Life
                Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                College of Medicine); available through Life
                Technologies."

ORIGIN
Query Match      92.0%; Score 127; DB 13; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 71
Db 1 TGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGGCGCCGACGACGCC 60

QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 131
Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGGACTGGGGCTGTCCGACTGACCTCGCC 120

QY 132 CTGTCCC 138
Db 121 CTGTCCC 127

RESULT 10
LOCUS      AI928896/c              550 bp    mRNA    linear    EST 23-AUG-1999
DEFINITION au65f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION  AI928896
VERSION     AI928896.1 GI:5664860
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 550)

```


RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998K074642.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No. 972)
<http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972> Contact: Ina Rolfes
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGAAACAGCTATGAC.

FEATURES

source

```
1. 468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998K074642 ; IMAGE:1894398"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta 8to9weeks 2NBP8to9w"
/notes="Organ: placenta; Vector: p77T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTCGGAGCGCGCGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
```

ORIGIN

```
Query Match      90.6%; Score 125; DB 13; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTCTACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 73
Dbb 1 GCTCTACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 60

QY 74 CGGCGCAGCCACCATGTAGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCT 133
Dbb 61 CGGCGCAGCCACCATGTAGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCT 120

QY 134 GTCCC 138
Dbb 121 GTCCC 125
```

RESULT 13

```
AI929147
LOCUS      433 bp mRNA linear EST 23-AUG-1999
DEFINITION au65f07.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
(HUMAN); mRNA sequence.
ACCESSION  AI929147
VERSION     AI929147.1 GI:5665111
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 433)
AUTHORS     Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,F., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
```

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco.

FEATURES

source

```
1. 433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519653"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/notes="Organ: brain; Vector: pBluescript SK (Stratagene);
Site_1: SstI; Site_2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence:
5'-GAGAGAGAGAGAGCTCAAGGATCCTTAATTAAATTATCCGCCGCCGCC-3'
and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was
size-selected for >0.5 kb inserts and has an average
insert size estimated at 1.2 kb. This library was
constructed using the CAP-trapper method for full-length
enrichment and has not undergone amplification. Library
was constructed by Dr. Claudio Schneider (LNCIB-Area
Science Park, Trieste, Italy)."
```

ORIGIN

```
Query Match      89.9%; Score 124; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 74
Dbb 1 CTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGCCAGCCACGCGCG 60

QY 75 GCGCCAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTG 134
Dbb 61 GCGCCAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTCGCCCTG 120

QY 135 TCCC 138
Dbb 121 TCCC 124
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RESULT 14

```
BQ932266
LOCUS      567 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT 8804926 Lupski sciatic nerve Homo sapiens cDNA clone
IMAGE:6197017 5', mRNA sequence.
ACCESSION  BQ932266
VERSION     BQ932266.1 GI:22347297
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 567)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM13606 row: g column: 02
High quality sequence stop: 566.

FEATURES
source

Location/Qualifiers
1..567
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6197017"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGGCTCCG-3' and 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Query Match 82.6%; Score 114; DB 13; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 TCGGAGAGCGCTCCGCGACAGCATAGTACTTCGCGCCCGACGCGCGCGCCAGCCA 84
Db 1 TCGGAGAGCGCTCCGCGCGACAGCATAGTACTTCGCGCCCGACGCGCGCGCCAGCCA 60

QY 85 CCATCTAGGTAAACAGACGCTGGGGCTGTCGGGACTGACCTCGCCCTGTCCC 138
Db 61 CCATCTAGGTAAACAGACGCTGGGGCTGTCGGGACTGACCTCGCCCTGTCCC 114

RESULT 15
BQ886097

LOCUS BQ886097 1123 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8673508 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6199943 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ886097.1 GI:22278111
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1123)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE

AUTHORS NIH-MGC
TITLE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
JOURNAL DNA Sequencing by: Agencourt Bioscience Corporation
COMMENT Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM13613 row: p column: 24
High quality sequence start: 90
High quality sequence stop: 266.

FEATURES
source

Location/Qualifiers
1..1123

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6199943"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGGCTCCG-3' and 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Query Match 77.4%; Score 106.8; DB 13; Length 1123;
Best Local Similarity 90.6%; Pred. No. 1.6e-16;
Matches 125; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGATAGTACTTCCCGC 60
Db 41 ACCGCCCCAGCGTCCGCTCACCCCTCGGAGACGCTCGCCCGACAG-ATTGTACTCGACGC 99

QY 61 CCAGCCAGCCCGCGCGCCGACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGAC 120
Db 100 CCAGCCAGCCCGCGCGCCGACCATGCTAGGTAAACAGCGAGTGGGGCTGTCCGGAC 159

QY 121 TGACCCCTCGCCCTGTCCC 138
Db 160 TGACCCCTCGCCCTGTCCC 177

Search completed: April 26, 2004, 15:45:52
Job time : 2165 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 59.5 Seconds
(without alignments)
1287.113 Million cell updates/sec

Title: US-09-645-590-1
Perfect score: 138
Sequence: 1 accccatccgtggtctca.....actgaccctcgccctgtccc 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	551	3	US-08-994-946A-5
2	138	100.0	551	4	US-09-291-994-5
3	136.4	98.8	1588	4	US-09-976-594-625
4	113.2	82.0	122	4	US-09-621-976-8234
5	91	65.9	325	3	US-08-934-946A-1
6	91	65.9	325	4	US-09-291-994-1
7	52	37.7	247	3	US-08-994-946A-2
8	52	37.7	247	4	US-09-291-994-2
9	30.6	22.2	945	4	US-09-252-991A-14797
10	30.6	22.2	2550	4	US-09-252-991A-14954
11	30.2	21.9	1242	4	US-09-252-991A-9668
12	30.2	21.9	1518	4	US-09-252-991A-6357
13	30.2	21.9	1521	4	US-09-489-039A-6357
14	30.2	21.9	2511	4	US-09-252-991A-9746
15	30.2	21.9	2583	4	US-09-252-991A-9541
16	29.6	21.4	588	4	US-09-252-991A-6523
17	29.6	21.4	891	4	US-09-252-991A-6513
18	29.6	21.4	999	4	US-09-252-991A-14871
19	29.6	21.4	1608	4	US-09-252-991A-14491
20	29.2	21.2	670	4	US-09-009-816-3
21	29.2	21.2	1104	4	US-09-009-816-1
22	29.2	21.2	1108	4	US-09-800-729-42
23	29.2	21.2	1141	4	US-09-800-729-78
24	29.2	21.2	1237	4	US-09-800-729-80
25	28.8	20.9	2748	4	US-09-489-039A-1078
26	28.4	20.6	1247	1	US-08-278-729A-32
27	28.4	20.6	1247	1	US-08-155-343A-32

28	28.4	20.6	1247	1	US-08-406-672-32	Sequence 32, Appl
29	28.4	20.6	1247	1	US-08-643-563A-32	Sequence 32, Appl
30	28.4	20.6	1247	1	US-08-643-763A-32	Sequence 32, Appl
31	28.4	20.6	1247	1	US-08-462-623-32	Sequence 32, Appl
32	28.4	20.6	1247	1	US-08-451-953A-32	Sequence 32, Appl
33	28.4	20.6	1247	2	US-08-445-468A-32	Sequence 32, Appl
34	28.4	20.6	1247	2	US-08-461-397A-32	Sequence 32, Appl
35	28.4	20.6	1247	3	US-08-912-088-32	Sequence 32, Appl
36	28.4	20.6	1247	3	US-08-278-730A-32	Sequence 32, Appl
37	28.4	20.6	1247	3	US-08-445-467-32	Sequence 32, Appl
38	28.4	20.6	1247	3	US-08-480-515A-32	Sequence 32, Appl
39	28.4	20.6	1247	4	US-09-170-936-32	Sequence 32, Appl
40	28.4	20.6	1247	4	US-08-461-113-32	Sequence 32, Appl
41	28.4	20.6	1247	4	US-08-456-033-32	Sequence 32, Appl
42	28.4	20.6	1247	4	US-08-643-321-30	Sequence 32, Appl
43	28.4	20.6	1247	5	PCT-US93-07190-32	Sequence 30, Appl
44	28.4	20.6	1247	5	PCT-US93-07231-32	Sequence 32, Appl
45	28.4	20.6	1247	5	PCT-US93-08742-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-994-946A-5
; Sequence 5, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,946A
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 87..170
; NAME/KEY: CDS
; LOCATION: 87..377

US-08-994-946A-5

Query Match	100.0%;	Score 138;	DB 3;	Length 551;
Best Local Similarity	100.0%;	Pred. No. 3.6e-32;		
Matches 138;	Conservative	0;	Mismatches	0;
Indels				
Gaps				

[illegible]

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RESULT 2
US-09-291-994-5
; Sequence 5, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; TITLE OF INVENTION: Y Gene.
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 551

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Query Match	100.0%;	Score 138;	DB 4;	Length 551;
Best Local Similarity	100.0%;	Pred. No. 3.6e-32;		
Matches 138;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGC	CGC	60	
1	ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGC	CGC	60	
61	CCAGCCACGCGCGCGCCACGACCATGCTAGGTAACAAGCGACTGGGGCTGTCCG	GAC	120	
61	CCAGCCACGCGCGCGCCACGACCATGCTAGGTAACAAGCGACTGGGGCTGTCCG	GAC	120	
121	TGACCCCTGGCCCTGTCC	138		
121	TGACCCCTGGCCCTGTCC	138		

RESULT 3
US-09-976-594-625
; Sequence 625 Application US/09976594
; Patent No. 6673813
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchholdt, Jenny
; APPLICANT: Buchholdt, Jenny

```

; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 625
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673349
; NAME/KEY: unsure
; LOCATION: 7, 19, 25, 33, 45, 59, 88, 96,
; LOCATION: 221, 226, 232, 245, 264, 276,
; LOCATION: 363, 373, 377, 382, 395, 407,
; LOCATION: 504, 537, 551, 556, 583, 592,
; LOCATION: 738, 747, 751, 756, 762, 774,
; OTHER INFORMATION: a, t, c, g, or other
; US-09-976-594-625

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Query Match	98.8%;	Score 136.4;	DB 4;	Length 1588;
Best Local Similarity	99.3%;	Pred. NO. 1.2e-31;		
Matches 137;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ACCCATCCGCTGGCTCTCACCCCTTCGGAGACGCTGCGCCGACAGCATAGTACTTGCCGC	60	
Db	1031	ACCCCATCCGCTGGCTCTCACCCCTTCGGAGACGCTGCGCCGACAGCATAGTACTTGCCGC	1090	
Qy	61	CCAGCCACGCGCGCGCCACCCACCATGTTAGTGTAACAAGCGACTGGGCGCTGTCCGGAC	120	
Db	1091	CCAGCCACGCGCGCGCCACCCACCATGTTAGTGTAACAAGCGACCGGGCGCTGTCCGGAC	1150	
Qy	121	TGACCCCTGCGCCTGTGTCC	138	
Db	1151	TGACCCCTGCGCCTGTGTCC	1168	

```

RESULT 4
US-09-621-976-8234
; Sequence 8234, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8234
; LENGTH: 122
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8234

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Query Match	82.0%;	Score 113.2;	DB 4;	Length 122;
Best Local Similarity	94.3%;	Pred. NO. 6.3e-25;		
Matches 115; Conservative	2;	Mismatches 5;	Indels 0;	Gaps 0;
QY	1	ACCCATCGGTGGTCTCACCCCTCGAGAGCGTCGCCGACAGCATAGTACTTGCCGC	60	
Dd	1	ACCCATCGGTGGTCTCACCCCTCGAGAGCGTCGCCGACAGCATAGTACTTGCCGC	60	
QY	61	CCAGCCAGCCGCGCGCCAGCCACCTAGTAGTAACAAGCAGTGGGGTGTCGGAC	120	
Dd	61	CCAGCCAGCCGCGCGCCAGCCACCTAGTAGTAACAAGCAGTGGGGTGTCGGAC	120	
QY	121	TG 122		

```

Db      121 TG 122
||
RESULT 5
US-08-994-946A-1
; Sequence 1, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; APPLICATION DATA:
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-994-946A-1

Query Match      65.9%; Score 91; DB 3; Length 325;
Best Local Similarity 90.7%; Pred. No. 2.6e-18;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 60
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Db      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 269

QY      61 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTACACGCGACTG 107
        |||||||
Db      270 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTACACGCGCTG 316

RESULT 7
US-08-994-946A-2
; Sequence 2, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; APPLICATION DATA:
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-994-946A-1

Query Match      65.9%; Score 91; DB 3; Length 325;
Best Local Similarity 90.7%; Pred. No. 2.6e-18;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 60
        |||||||
Db      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGGCGC 269

QY      61 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTACACGCGACTG 107
        |||||||
Db      270 CCAGCCACGCCCGCGCGCCGACCATGCTAGGTACACGCGCTG 316

RESULT 6
US-09-291-994-1
; Sequence 1, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine

```

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 ATGCTAGTAAACAGCGACTGGGCTGTCGGAGCTGACCTCGCCCTGTCCTCC 138
|||||
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCGGAGCTGACCTCGCCCTGTCCTCC 81
|||||

RESULT 8
US-09-291-994-2
; Sequence 2, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulou, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ulla-Mari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; TITLE OF INVENTION: Y Gene.
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-994-2

Query Match 37.7%; Score 52; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 8.3e-07; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 ATGCTAGTAAACAGCGACTGGGCTGTCGGAGCTGACCTCGCCCTGTCCTCC 138
|||||
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCGGAGCTGACCTCGCCCTGTCCTCC 81
|||||

RESULT 9
US-09-252-991A-14797/c
; Sequence 14797, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14797
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14797

Query Match 22.2%; Score 30.6; DB 4; Length 945;
Best Local Similarity 51.9%; Pred. No. 2.1; Indels 0; Gaps 0;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGCATAGTATTGCGGC 60
|||||
Db 611 ACCCGCGGGTGGCAACCGAGAGAGCTTGACATCGCCCGCTGCGCTCGCCGAGCATC 552
|||||

QY 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGCTGTCGGAC 120
|||||
Db 551 GCCGGCAGCGCGCTCGGCAACCAACAGGTGGGAGCAGCGAAGCCCGAGCTCGGCC 492
|||||

QY 121 TGACCTCGCCCT 133
|||||
Db 491 TCAATCTGTCCT 479
|||||

RESULT 10
US-09-252-991A-14954
; Sequence 14954, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14954
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14954

Query Match 22.2%; Score 30.6; DB 4; Length 2550;
Best Local Similarity 51.9%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 69; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ACCCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGAGCATAGTATTGCGGC 60
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Db 1890 ACCCGCGGGTGGCAACCGAGAGCTTGACATCGCCCGCTGCGCTCGCCGAGCATC 1939
|||||

QY 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGCTGTCGGAC 120
|||||
Db 1940 GCCGGCAGCGCGCTCGGCAACCAACAGGTGGGAGCAGCGAAGCCCGAGCTCGGCC 1999
|||||

QY 121 TGACCTCGCCCT 133
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Db 2000 TCAATCTGTCCT 2012
|||||

RESULT 11
US-09-252-991A-9668/c
; Sequence 9668, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9668
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9668

Query Match 21.9%; Score 30.2; DB 4; Length 1242;
Best Local Similarity 53.9%; Pred. No. 2.8; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGAGCTCGCCGACGAGCATAGTACTTTCGCCGCCAGCCAGCCGCGCCAGCC 83
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Db 947 CTCGAGAGCCCGCCAGACGGCTCTCGATATGGCCAGCGCCGCGCCAGCTTCCTGGCC 888

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTCTCCGAGCTGACCTCGCCCTGTGCC 138

Db 887 AACATGAGCCAGAGATCCGACGCCGCTGAACGGCCTGCTCGGATGCTCTCGC 833

RESULT 12

US-09-489-039A-6357/c
; Sequence 6357, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6357
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6357

Query Match 21.9%; Score 30.2; DB 4; Length 1518;
Best Local Similarity 60.2%; Pred. No. 2.9;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2 CCCATCCGCTGCTCTCACCCCTCGAGAGCGCTCGGCGGCGGAGCAGCATAGTACTTGGCGCC 61

Db 1056 CCCATCAGCTCGTTCATCCAGCGCGCGACCCGCGGCGAAAGCGCTGAGCTTGCTTT 997

QY 62 CAGCCAGCGCGCGCGCCAGCCA 84

Db 996 CAGCAGGCCAGTACCGCATCCA 974

RESULT 13

US-09-252-991A-9746/c
; Sequence 9746, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9746
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9746

Query Match 21.9%; Score 30.2; DB 4; Length 1521;
Best Local Similarity 53.9%; Pred. No. 2.9;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCGCGCGCGCCAGCC 83

Db 1506 CTCGAGAGACCCGCGCAGACCGCTCTCGATATGGCCCGCGCGCGCGCTTCCTGGCC 1447

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTCTCGGAGCTGACCTCGCCCTGTGCC 138

Db 1446 AACATGAGCCAGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1392

RESULT 14

US-09-252-991A-9494
; Sequence 9494, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9494
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9494

Query Match 21.9%; Score 30.2; DB 4; Length 2511;
Best Local Similarity 53.9%; Pred. No. 3.1;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCGCGCGCGCCAGCC 83

Db 932 CTCGAGAGACCCGCGCAGACCGCTCTCGATATGGCCCGCGCGCGCGCTTCCTGGCC 991

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAGCTGACCTCGCCCTGTGCC 138

Db 992 AACATGAGCCAGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1046

RESULT 15

US-09-252-991A-9541
; Sequence 9541, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9541
; LENGTH: 2583
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9541

Query Match 21.9%; Score 30.2; DB 4; Length 2583;
Best Local Similarity 53.9%; Pred. No. 3.1;
Matches 62; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 24 CTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCAGCCAGCCGCGCGCGCCAGCC 83

Db 1096 CTCGAGAGACCCGCGCAGACCGCTCTCGATATGGCCCGCGCGCGCGCTTCCTGGCC 1155

QY 84 ACCATGCTAGGTAAACAGCGACTGGGCTGTCCGAGCTGACCTCGCCCTGTGCC 138

Db 1156 AACATGAGCCAGAGATCCGACGCCGCTGAACGGCTGTCTCGGCATGCTCTCGC 1210

Search completed: April 26, 2004, 15:48:01

Job time : 60.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:26 ; Search time 245 Seconds
(without alignments)

2539.553 Million cell updates/sec

Title: US-09-645-590-1

Perfect score: 138

Sequence: 1 accacatccgctgctctca.....actgacctcgccctgtccc 138

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Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

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Minimum DB seq length: 0

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 17: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	138	100.0	551	14	US-10-002-048A-1
4	138	100.0	551	15	US-10-002-048A-1
5	138	100.0	551	15	US-10-236-903-5
6	138	100.0	551	15	US-10-017-273A-1
7	124.8	90.4	969	15	US-10-191-997-94
8	111	80.4	553	15	US-10-036-542-16
9	111	80.4	553	9	US-10-036-542-41
10	111	80.4	559	15	US-09-925-300-100
11	91	65.9	325	13	US-10-036-542-42
12	91	65.9	325	13	US-10-069-129-1
13	91	65.9	325	14	US-10-002-048A-3
14	91	65.9	325	15	US-10-236-903-1
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	16	89.4	64.8	496	10	US-09-918-995-2739	Sequence 2739, App
	17	62.8	45.5	417	15	US-10-205-823-288	Sequence 288, Appli
	18	52	37.7	247	13	US-10-069-129-2	Sequence 2, Appli
	19	52	37.7	247	14	US-10-002-048A-4	Sequence 4, Appli
	20	52	37.7	247	15	US-10-236-903-2	Sequence 2, Appli
	21	51	37.0	1021	16	US-10-321-039-55	Sequence 55, Appli
	22	33.4	24.2	2175	13	US-10-425-114-33220	Sequence 33220, A
	23	32.8	23.8	1020	15	US-10-156-761-7175	Sequence 7175, Ap
	24	32.8	23.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
	25	32.4	23.5	2573	16	US-10-108-260A-672	Sequence 672, App
C	26	32.4	23.5	32329	13	US-10-374-903A-1	Sequence 1, Appli
	27	32	23.2	867	15	US-10-156-761-1834	Sequence 1834, Ap
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	29	31.6	22.9	7185	15	US-10-329-079-48	Sequence 48, Appli
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C	31	31.2	22.6	440	15	US-10-184-644-202	Sequence 202, App
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C	34	31	22.5	1029	13	US-10-282-122A-11962	Sequence 11962, A
C	35	31	22.5	1487	16	US-10-369-493-43101	Sequence 43101, A
	36	31	22.5	13416	15	US-10-205-032-11	Sequence 11, Appli
	37	31	22.5	60196	15	US-10-205-032-1	Sequence 1, Appli
	38	30.8	22.3	866	13	US-10-027-632-8562	Sequence 8562, Ap
	39	30.8	22.3	866	13	US-10-027-632-8563	Sequence 8563, Ap
	40	30.8	22.3	866	16	US-10-027-632-8562	Sequence 8562, Ap
	41	30.8	22.3	866	16	US-10-027-632-8563	Sequence 8563, Ap
C	42	30.8	22.3	957	16	US-10-260-238-948	Sequence 948, App
	43	30.8	22.3	6432	15	US-10-329-079-10	Sequence 10, Appli
	44	30.8	22.3	37360	15	US-10-329-079-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1

US-09-969-708-592
; Sequence 592, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 592
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-592

Query Match	100.0%;	Score 138;	DB 9;	Length 551;
Best Local Similarity	100.0%;	Pred. No. 2e-35;		
Matches 138;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	ACCCATCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGATAGTACTTGC	60	
QY	61	CCAGCCACGCCCGCGCGCGAGCGATCTAGGTAAAGCGACTGGGGCTTC	120	
Db	61	CCAGCCACGCCCGCGCGCGAGCGATCTAGGTAAAGCGACTGGGGCTTC	120	

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QY 121 TGACCTCGCCCTGTCCC 138
      |||||
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 2
US-10-069-129-5
; Sequence 5, Application US/10069129
; Publication No. US20030224362A1
; GENERAL INFORMATION:
; APPLICANT: Jussi Kauphanen, Matti Karvonen, Ullamari Pesonen, Markku Koulu, Matti
; APPLICANT: Uusitupa
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Alcoholism Based on Leucine7 Polymorphism in the Pr
; TITLE OF INVENTION: Neuropeptide
; TITLE OF INVENTION: Y Gene, and Methods for the prevention and Treatment of Alcoholi
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/069,129
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)..(377)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (87)..(170)
US-10-069-129-5

Query Match 100.0%; Score 138; DB 13; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60

QY 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTCCC 138
      |||||
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 3
US-10-002-048A-1
; Sequence 1, Application US/10002048A
; Publication No. US20020182616A1
; GENERAL INFORMATION:
; APPLICANT: Wahlestedt, Claes
; APPLICANT: Ding, Bo
; TITLE OF INVENTION: Single Nucleotide Polymorphisms
; FILE REFERENCE: 10806-143
; CURRENT APPLICATION NUMBER: US/10/002,048A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: SE 0004035-2
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 551
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (87)..(380)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (87)..(170)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank/K01911
; DATABASE ENTRY DATE: 1995-01-07
US-10-002-048A-1

Query Match 100.0%; Score 138; DB 14; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60

QY 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTCCC 138
      |||||
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 4
US-10-236-903-5
; Sequence 5, Application US/10236903
; Publication No. US20030093821A1
; GENERAL INFORMATION:
; APPLICANT: Hormos Medical Oy, Ltd.
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant Prepro-Neuropeptide Y, a Mutant
; TITLE OF INVENTION: Peptide, and Uses Thereof
; FILE REFERENCE: 2328-126
; CURRENT APPLICATION NUMBER: US/10/236,903
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/472,188
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 08/994,946
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)..(377)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (87)..(170)
US-10-236-903-5

Query Match 100.0%; Score 138; DB 15; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTACTTGGCGC 60

QY 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCAGCCGCGCGCGGAGCAGCCATGCTAGGTAAACAGGACTGGGGCTGTCCGGAC 120
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QY 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 5
US-10-017-273A-1
; Sequence 1, Application US/10017273A
; Publication No. US20030119714A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Naylor, Alasdair M.
; APPLICANT: Van Der Graaf, Pieter H
; APPLICANT: Wayman, Christopher P.
; TITLE OF INVENTION: Treatment of Male Sexual Dysfunction
; FILE REFERENCE: P22013
; CURRENT APPLICATION NUMBER: US/10/017,273A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/265,358
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: GB 0030647.2
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 0108730.3
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: GB 0120679.6
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 09/905,846
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/291,722
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 09/895,367
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-273A-1

Query Match 100.0%; Score 138; DB 15; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60
Db 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60

QY 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 6
US-10-191-997-94
; Sequence 94, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: NPY: Acc. No. US20030207834A1 K01911
US-10-191-997-94

Query Match 100.0%; Score 138; DB 16; Length 551;
Best Local Similarity 100.0%; Pred. No. 2e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60
Db 1 ACCCCATCCGCTGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCCG 60

QY 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCCGACCCATGCTAGGTAACAAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCCCTGCCCTGTGCC 138
Db 121 TGACCCCTGCCCTGTGCC 138

RESULT 7
US-10-036-542-16
; Sequence 16, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002p1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (118)..(118)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (254)..(255)
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (839)..(839)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (897)..(897)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-036-542-16

Query Match 90.4%; Score 124.8; DB 15; Length 969;
Best Local Similarity 96.9%; Pred. No. 3.8e-31;
Matches 126; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 9 CGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCAC 68
|||
Db 250 CGAGNNCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCAC 309
|||
QY 69 GCCCGGGCCAGCCACCATGCTAGTTAACAGCGACTGGGGCTGTCGGACTGACCCCTC 128
|||
Db 310 GCCCGGGCCAGCCACCATGCTAGTTAACAGCGACTGGGGCTGTCGGACTGACCCCTC 369
|||
QY 129 GCCCTGTCCC 138
|||
Db 370 GCCCTGTCCC 379
|||

RESULT 8
US-10-036-542-41
; Sequence 41, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-036-542-41

Query Match 80.4%; Score 111; DB 15; Length 553;
Best Local Similarity 99.2%; Pred. No. 1.2e-26;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 16 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCACGCGCGG 75
Db 1 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCACGCGCGG 60
|||
QY 76 CGCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGACTGACCCCTGCTGT 135
|||
Db 61 CGCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGACTGACCCCTGCTGT 119
|||
QY 136 CCC 138
|||

Db 120 CCC 122

RESULT 9
US-09-925-300-100
; Sequence 100, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (583)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (599)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-100

Query Match 80.4%; Score 111; DB 9; Length 599;
Best Local Similarity 99.2%; Pred. No. 1.2e-26;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 16 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCACGCGCGG 75
|||
Db 14 TCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTATTGCGGCCCGCCACGCGCGG 73
|||
QY 76 CGCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGACTGACCCCTGCTGT 135
|||
Db 74 CGCCA-CCCATGCTAGGTAAACAAGCGACTGGGGCTGTCGGACTGACCCCTGCTGT 132
|||
QY 136 CCC 138
|||
Db 133 CCC 135
|||

RESULT 10
US-10-036-542-42
; Sequence 42, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06

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; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (583)..(584)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (599)..(599)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-036-542-42

Query Match      80.4%; Score 111; DB 15; Length 599;
Best Local Similarity 99.2%; Pred. No. 1.2e-26;
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 16 TCTCACCCTCGGAGAGCTCGCCGACAGCATAGTACTTCCCGCCGACGACGCGCCGCG 75
Db 14 TCTCACCCTCGGAGAGCTCGCCGACAGCATAGTACTTCCCGCCGACGACGCGCCGCG 73
QY 76 CGCCAGCCACCATCTAGGTAAACAGGACTGGGGCTGTCCGGACTGACCTCGCCCTGT 135
Db 74 CGCA-CCACCATCTAGGTAAACAGGACTGGGGCTGTCCGGACTGACCTCGCCCTGT 132
QY 136 CCC 138
Db 133 CCC 135

RESULT 11
US-10-069-129-1
; Sequence 1, Application US/10069129
; Publication No. US20030224362A1
; GENERAL INFORMATION:
; APPLICANT: Jussi Kauhane, Matti Karvonen, Ullamari Pesonen, Markku Koulu, Matti
; APPLICANT: Uusitupa
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Alcoholism Based on Leucine7 to Proline 7 Polymorphism in the Pr
; TITLE OF INVENTION: Neuropeptide
; TITLE OF INVENTION: Y Gene, and methods for the prevention and Treatment of Alcoholi
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/069,129
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-069-129-1

Query Match      65.9%; Score 91; DB 13; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 269

QY 61 CCAGCCAGCCCGCGCGCCGACGACCATGCTAGGTAAACAGGACTG 107
Db 270 CCAGCCAGCCCGCGCGCCGACGACCATGCTAGGTAAACAGGACTG 316

RESULT 12
US-10-002-048A-3
; Sequence 3, Application US/10002048A
; Publication No. US200020182616A1
; GENERAL INFORMATION:
; APPLICANT: Wahlestedt, Claes
; APPLICANT: Ding, Bo
; TITLE OF INVENTION: Single Nucleotide Polymorphisms
; FILE REFERENCE: 10806-143
; CURRENT APPLICATION NUMBER: US/10/002,048A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: SE 0004035-2
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 325
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: prim_transcript
; LOCATION: (210)..(325)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank/M14295
; DATABASE ENTRY DATE: 1995-01-08
US-10-002-048A-3

Query Match      65.9%; Score 91; DB 14; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 269

QY 61 CCAGCCAGCCCGCGCGCCGACGACCATGCTAGGTAAACAGGACTG 107
Db 270 CCAGCCAGCCCGCGCGCCGACGACCATGCTAGGTAAACAGGACTG 316

RESULT 13
US-10-236-903-1
; Sequence 1, Application US/10236903
; Publication No. US20030093821A1
; GENERAL INFORMATION:
; APPLICANT: Hormos Medical Oy, Ltd.
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant Prepro-Neuropeptide Y, a Mutant
; TITLE OF INVENTION: Peptide, and Uses Thereof
; FILE REFERENCE: 2328-126
; CURRENT APPLICATION NUMBER: US/10/236,903
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/472,188
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 08/994,946
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-236-903-1

Query Match      65.9%; Score 91; DB 15; Length 325;
Best Local Similarity 90.7%; Pred. No. 3.9e-20;
Matches 97; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 60
Db 210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACGATAGTACTTGGCGC 269
```

Qy 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACTG 107

p6 270 CCAGCCACGCCCGCGCGCCAGCCACCGTGAAGTGTACTAGACCCGCTCTG 316

RESULT 14

```

US-10-027-632-127333/c
; Sequence 127333, Application US/10027632
; Publication No. US2002019837nAI
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127333
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-127333

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Query Match 65.9%; Score 91; DB 13; Length 646;
Best Local Similarity 90.7%; Pred. No. 3.8e-20;
Matches 97: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACCCCATCGCTGGCTCTCAACCCCTCGAGACGCTGCCCGACAGCATAGTACTTGGCCG 60
DB 391 ACCCCATCGCTGGCTCTCAACCCCTCGGAGACGCTGCCCGACAGCATAGTACTTGGCCG 332
QY 61 CCAGCCAGCCCGCGCGCCAGCCACCTACTAGTAAACAGGACTG 107
DB 331 CCAGCCAGCCCGCGCGCCAGCCACCTGAGTGTACGACCGCTGTG 285

DEPT. T 15

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US-10-027-632-127333/c
; Sequence 127333, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 860 Seconds
(without alignments)
6955.045 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb_pat.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	136.4	98.8	551	6	AXI38816	AXI38816 Sequence
3	136.4	98.8	551	6	AXI39001	AXI39001 Sequence
4	136.4	98.8	551	6	AXI39420	AXI39420 Sequence
5	136.4	98.8	551	6	AX337554	AX337554 Sequence
6	136.4	98.8	551	6	AX463054	AX463054 Sequence
7	136.4	98.8	551	6	BD015786	BD015786 Compound
8	136.4	98.8	551	6	BD015859	BD015859 Compound
9	136.4	98.8	551	6	BD103561	BD103561 Variant p
10	136.4	98.8	551	9	HUMNPY	K01911 Human neuro
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12	136.4	98.8	568	9	BC029497	BC029497 Homo sapi
13	136.4	98.8	122	6	AR416737	AR416737 Sequence
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15	89.4	64.8	325	6	ARI76715	ARI76715 Sequence
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19	88.6	64.2	182634	9	AC142353	AC142353 Pan trogl
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26	61.6	44.6	539	10	RATNPY	M15860 Rat neurope
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28	61.4	44.5	483	6	AX305379	AX305379 Sequence
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31	50.4	36.5	247	6	ARI76716	ARI76716 Sequence
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35	49	35.5	130	6	BD033295	BD033295 Sequence
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37	40.8	29.6	269	10	AF286198	AF286198 Mus muscu
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39	40.8	29.6	483	10	AF273788	AF273788 Rat neurope
40	40.8	29.6	2680	10	RATNPY01	M15792 Rat neurope
41	40.8	29.6	8102	10	AF392060	AF392060 Rattus no
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ALIGNMENTS

RESULT 1
ARI76719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

ARI76719
Sequence 5 from patent US 6312898.
ARI76719
ARI76719.1 GI:17919074
Unknown.
Unclassified.
1 (bases 1 to 551)
Koulu, M., Karvonen, M., Pesonen, U. and Uusitupa, M.
Diagnosis of a person's risk of developing atherosclerosis or
diabetic retinopathy based on leucine 7 to proline 7 polymorphism
in the prepro-neuropeptide Y gene

551 bp
DNA
linear
PAT 17-DEC-2001

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JOURNAL Patent: US 6312898-A 5 06-NOV-2001;
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QY 121 TGACCCCTGCGCCCTGTCCC 138
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RESULT 2
AX138816 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097706.
ACCESSION AX138816
VERSION AX138816.1 GI:14274563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Phosphodiesterase inhibitors for the treatment of female sexual
JOURNAL dysfunction
Patent: EP 1097706-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
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RESULT 3
AX139001 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097707.
ACCESSION AX139001
VERSION AX139001.1 GI:14274691
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Np inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 2.3e-22;
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QY 121 TGACCCCTGCGCCCTGTCCC 138
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RESULT 4
AX139420 551 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Np inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
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RESULT 5
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LOCUS
DEFINITION Sequence 8 from Patent EP1097719.
ACCESSION AX139420
VERSION AX139420.1 GI:14275073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Np inhibitors for the treatment of female sexual dysfunction
JOURNAL Patent: EP 1097719-A 8 09-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
FEATURES Location/Qualifiers
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AX337554
LOCUS AX337554 551 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 8063 from Patent WO0194629.
ACCESSION AX337554
VERSION AX337554.1 GI:18128273
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrihan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 8063 13-DEC-2001;
Avalon Pharmaceuticals (US)
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source Location/Qualifiers
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QY 121 TGACCCCTCGCCCTGTGCC 138
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Db 121 TGACCCCTCGCCCTGTGCC 138
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LOCUS AX463054 551 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 1 from Patent WO0247670.
ACCESSION AX463054
VERSION AX463054.1 GI:21886069
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Naylor, A.M., van der Graaf, P.H. and Wayman, C.P.
TITLE Treatment of male sexual dysfunction
JOURNAL Patent: WO 0247670-A 1 20-JUN-2002;
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LOCUS BD015786 551 bp DNA linear PAT 27-AUG-2002
DEFINITION Compound for treatment of female sexual dysfunction.
ACCESSION BD015786
VERSION BD015786.1 GI:22556923
KEYWORDS JP 2001206855-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
REFERENCE
AUTHORS Maw, G.N. and Wayman, C.P.
TITLE Compound for treatment of female sexual dysfunction
JOURNAL Patent: JP 2001206855-A 4 31-JUL-2001;
PRIZER INC
COMMENT
OS Homo sapiens (human)
PN JP 2001206855-A/4
PD 31-JUL-2001
PF 08-NOV-2000 JP 2000339905
PR 08-NOV-1999 GB 9926437.6, 18-FEB-2000 GB 0004021.2 PR
26-MAY-2000 GB 0013001.3, 05-JUL-2000 GB 0016563.9 PR
12-JUL-2000 GB 0017141.3
PI GRAHAM NIGEL MAW, CHRISTOPHER PETER WAYMAN
PC A61K45/00, A61K31/122, A61K31/165, A61K31/17, A61K31/18, A61K31/19,
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DEFINITION  Compound for treatment of female sexual dysfunction.
ACCESSION   BD015859
VERSION     BD015859.1  GI:22556996
KEYWORDS    JP 2001213802-A/4.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Maw G.N. and Wayman C.P.
TITLE       Compound for treatment of female sexual dysfunction
JOURNAL     Patent: JP 2001213802-A 4 07-AUG-2001;
            PFIZER INC
COMMENT     OS Homo sapiens (human)
            PN JP 2001213802-A/4
            PD 07-AUG-2001
            PR 08-NOV-2000 JP 2000339853
            PR 08-NOV-1999 GB 9926437.6,18-FEB-2000 GB 0004021.2 PR
            26-MAY-2000 GB 0013001.3,05-JUL-2000 GB 0016563.9 PR
            12-JUL-2000 GB 0017141.3
            PI GRAHAM NIGEL MAW,CHRISTOPHER PETER WAYMAN
            PC A61K45/00,A61K31/19,A61K31/192,A61K31/4015,A61K31/433,A61K31/
            PC 44,A61P15/00,
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            C07D207/27,C07D213/75,C07D285/135,G01N33/15,G01N33/50//C07C233/ PC
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RESULT 9
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LOCUS       BD103561             551 bp    RNA        linear    PAT 27-AUG-2002
DEFINITION  Variant preneuropeptide Y, DNA molecule encoding variant signal
            peptide and utilization of the same.
ACCESSION   BD103561
VERSION     BD103561.1  GI:22649135
KEYWORDS    JP 2001526296-A/5.
SOURCE      unidentified
            unclassified.
            1  (bases 1 to 551)

REFERENCE

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AUTHORS     Koulu,M., Karvonen,M., Pesonen,U. and Uusitupa,M.
TITLE       Variant preneuropeptide Y, DNA molecule encoding variant signal
            peptide and utilization of the same
JOURNAL     Patent: JP 2001526296-A 5 18-DEC-2001;
            HORMOS MEDICAL OY LTD
COMMENT     OS Unidentified
            PN JP 2001526296-A/5
            PD 18-DEC-2001
            PR 16-DEC-1998 JP 2000525455
            PR 19-DEC-1997 US 08/994946
            PI MARKKU KOULU,MATTI KARVONEN ULLAMARI PESONEN MATTI UUSITUPA PC
            C07K14/575,A01K67/027,A61K38/00,A61K38/22,A61K48/00,A61P3/06, PC
            A61P43/00,
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            C12P21/08,
            PC A61K37/02,A61K37/24,C12N5/00,C12N15/00
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            CC Topology: Linear;
            CC Variant preneuropeptide Y, DNA molecule encoding variant
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Best Local Similarity 99.3%; Pred. No. 2.3e-22;
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QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCCGC 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCCGC 60
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGTTAAACAGCGACCGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATGCTAGTTAAACAGCGACTGGGGCTGTCCGGAC 120
QY 121 TGACCTCGCCCTGTGCC 138
Db 121 TGACCTCGCCCTGTGCC 138

RESULT 10
HUMNPY
LOCUS       Human neuropeptide Y (NPY) mRNA, complete cds.
DEFINITION  K01911
ACCESSION   K01911
VERSION     K01911.1  GI:189273
KEYWORDS    neuropeptide Y.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Minth,C.D., Bloom,S.R., Polak,J.M. and Dixon,J.E.
TITLE       Cloning, characterization, and DNA sequence of a human cDNA
            encoding neuropeptide tyrosine
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 81 (14), 4577-4581 (1984)
MEDLINE     84272678
PUBMED      6589611
COMMENT     Original source text: Human pheochromocytoma, cDNA to mRNA, clone
            pNP13-75.
            Neuropeptide Y (NPY) is one of the most abundant peptides in the
            mammalian nervous system, and its extensive distribution suggests a
            neuro-transmitter or -modulator role. NPY is also found in some
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            Location/Qualifiers

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RESULT 11
G18330
LOCUS
DEFINITION SW51475 Eric D. Green Homo sapiens STS genomic, sequence tagged
site
G18330
VERSION G18330.1 GI:1222787
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 551)
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
Leckie,M.P. and Green,E.D.
Buffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
97189344
MEDLINE
PUBMED
9037602
REFERENCE 2 (bases 1 to 551)
Green,E.D.
AUTHORS Human chromosome 7 STSs (1997)
TITLE Unpublished (1997)
JOURNAL
SYNOPSIS: NPY
GDB: GDB:3754247
GDB_DSEG: NPY

```

Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CCACCATCTTACCAATG
Primer B: GACAAAGGAAAACATTGCAG
STS size: 60
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 55 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600

Protocol:
Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

This STS was developed from sequence determined by another investigator. See GenBank record: K01911 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].

FEATURES

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ORIGIN

Query Match 98.8%; Score 136.4; DB 11; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.3e-22;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 60
Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGCGCTCGCCGACGACATAGTACTTGGCGC 60
Qy 61 CCAGCCAGCCCGCGCGCCAGCCACCATCTAGTAAAGCGACCGGGGCTGTCCGAC 120
Db 61 CCAGCCAGCCCGCGCGCCAGCCACCATCTAGTAAAGCGACCGGGGCTGTCCGAC 120
Qy 121 TGACCTCGCCCTGTCCC 138
Db 121 TGACCTCGCCCTGTCCC 138

RESULT 12

BC029497
LOCUS
DEFINITION BC029497 Homo sapiens neuropeptide Y, mRNA (cDNA clone MGC:33138 IMAGE:5278692), complete cds.
568 bp mRNA linear PRI 06-OCT-2003

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ACCESSION      BC029497
VERSION        BC029497.1  GI:20809582
KEYWORDS       MGC.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 568)
AUTHORS        Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
               Klatschner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
               Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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               Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
               Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
               Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
               Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
               Generation and initial analysis of more than 15,000 full-length
               human and mouse cDNA sequences
               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
               22388257
               12477932
               2 (bases 1 to 568)
               Strausberg,R.
               Direct Submission
               Submitted (01-MAY-2002) National Institutes of Health, Mammalian
               Gene Collection (MGC), Cancer Genomics Office, National Cancer
               Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
               USA
               NIH-MGC Project URL: http://mgc.nci.nih.gov
               Contact: MGC help desk
               Email: cgabps@mail.nih.gov
               Tissue procurement: Miklos Palkovits, M.D., Ph.D.
               cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
               Toshiyuki and Piero Carninci (RIKEN)
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Sequencing Group at the Stanford Human Genome
               Center, Stanford University School of Medicine, Stanford, CA 94305
               Web site: http://www-shgc.stanford.edu
               Contact: (Dickson, Mark) mcd@paxil.stanford.edu
               Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
               R. M.
               Clone distribution: MGC clone distribution information can be found
               through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
               Series: IRAC Plate: 48 Row: h Column: 4
               This clone was selected for full length sequencing because it
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               AUTHORS
               Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
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               JOURNAL
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               BD112290
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               JP 2002010789-A/4367.
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               SOURCE

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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 122)			
TITLE	Edwards, J.B.D.M., Jobert, S. and Giordano, J.B.			
JOURNAL	EST and encoded human protein			
COMMENT	Patent: JP 2002010789-A 4367 15-JAN-2002; GENSET CORP			
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	PN	JP 2002010789-A/4367		
	PD	15-JAN-2002		
	PF	07-AUG-2000 JP 2000280989		
	PR	05-AUG-1999 US 60/147499		
	PI	JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE		
	GIORDANO			
	PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21,		
	PC	C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, C12N5/00, PC		
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ACCESSION	AR176715			
VERSION	AR176715.1 GI:17919070			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 325)			
AUTHORS	Koulu, M., Karvonen, M., Pesonen, U. and Uusitupa, M.			
TITLE	Diagnosis of a person's risk of developing atherosclerosis or diabetic retinopathy based on leucine 7 to proline 7 polymorphism in the prepro-neuropeptide Y gene			
JOURNAL	Patent: US 6312898-A 1 06-NOV-2001;			
FEATURES	US	6312898-A	1 06-NOV-2001;	
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	136.4	98.8	551	4	AAX84076 Human neu
9	136.4	98.8	551	6	ABL69726 Prostate
10	136.4	98.8	551	6	ABN84276 Human neu
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16	109.4	79.3	599	4	AAF72772 Human pro
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18	89.4	64.8	325	3	AAC60344 Human neu
19	89.4	64.8	325	6	AAL47340 Human neu
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ALIGNMENTS

RESULT 1
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AC AAL42206;
XX
DT 13-JUN-2002 (first entry)
XX
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XX
KW Human; ss; stress-induced neurotensin Y overproduction; NPY;
KW neurotransmitter; central nervous system; peripheral nervous system;
KW heart rate reduction; insulin secretion enhancement; NPY mRNA;
KW binding structure 2.
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OS Homo sapiens.
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WO200215941-A1.
28-FEB-2002.
31-JUL-2001; 2001WO-FI000687.
25-AUG-2000; 2000US-00645590.
(HORM-) HORMOS MEDICAL CORP.

```

XX PI Koululu M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;
XX XX
XX DR WPI; 2002-269319/31.
XX XX
XX PT Reducing stress-induced overproduction of neuropeptide Y (NPY) in an
XX PT individual useful for reducing heart rate and enhancing insulin
XX PT secretion.
XX PS Disclosure; Page 23; 45pp; English.
XX XX
XX CC The invention comprises a method for reducing stress-induced
XX CC overproduction of neuropeptide Y (NPY) in an individual. NPY is the most
XX CC abundant neuropeptide and an important neurotransmitter in the human
XX CC central and peripheral nervous system. The method of the invention is
XX CC useful for reducing constitutive overexpression of NPY in the endothelial
XX CC cells of an individual, in order to reduce the heart rate and enhance
XX CC insulin secretion. The method of the invention is also useful for
XX CC diagnosing susceptibility to stress-induced overproduction of NPY. The
XX CC present sequence represents binding structure 2 of the human NPY mRNA
XX XX
XX SQ Sequence 138 BP; 23 A; 61 C; 34 G; 20 T; 0 U; 0 Other;
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Query Match 98.8%; Score 136.4; DB 6; Length 138;
Best Local Similarity 99.3%; Pred. No. 2.4e-29;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 121 TGACCTCGCCCTGTCCC 138
Db 121 TGACCTCGCCCTGTCCC 138
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XX AC AAL42205;
XX XX
XX DT 13-JUN-2002 (first entry)
XX DE Human neuropeptide Y (NPY) mRNA sequence, binding structure 1.
XX KW Human; ss; stress-induced neuropeptide Y overproduction; NPY;
XX KW neurotransmitter; central nervous system; peripheral nervous system;
XX KW heart rate reduction; insulin secretion enhancement; NPY mRNA;
XX KW binding structure 1.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT stem_loop 10..38
XX FT /*tag= a
XX FT stem_loop 41..115
XX FT /*tag= b
XX FT stem_loop 117..137
XX FT /*tag= c
XX PN WO200215941-A1.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 31-JUL-2001; 2001WO-FI000687.
XX XX
XX PR 25-AUG-2000; 2000US-00645590.
XX XX

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PA (HORM-) HORMOS MEDICAL CORP.
XX XX
XX PI Koululu M, Karvonen M, Pesonen U, Uusitupa M, Kallio J;
XX XX
XX DR WPI; 2002-269319/31.
XX XX
XX PT Reducing stress-induced overproduction of neuropeptide Y (NPY) in an
XX PT individual useful for reducing heart rate and enhancing insulin
XX PT secretion.
XX PS Disclosure; Page 22; 45pp; English.
XX XX
XX CC The invention comprises a method for reducing stress-induced
XX CC overproduction of neuropeptide Y (NPY) in an individual. NPY is the most
XX CC abundant neuropeptide and an important neurotransmitter in the human
XX CC central and peripheral nervous system. The method of the invention is
XX CC useful for reducing constitutive overexpression of NPY in the endothelial
XX CC cells of an individual, in order to reduce the heart rate and enhance
XX CC insulin secretion. The method of the invention is also useful for
XX CC diagnosing susceptibility to stress-induced overproduction of NPY. The
XX CC present sequence represents binding structure 1 of the human NPY mRNA
XX XX
XX SQ Sequence 138 BP; 23 A; 61 C; 34 G; 20 T; 0 U; 0 Other;
XX
Query Match 98.8%; Score 136.4; DB 6; Length 138;
Best Local Similarity 99.3%; Pred. No. 2.4e-29;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGGACGATAGTACTTGGCGC 60
Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTGCCCGGACGATAGTACTTGGCGC 60
QY 61 CCAGCCACGCCCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCCCGCGCGCCAGCCACCATCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120
QY 121 TGACCTCGCCCTGTCCC 138
Db 121 TGACCTCGCCCTGTCCC 138
RESULT 3
AAX86051
ID AAX86051 standard; cDNA; 551 BP.
XX AC AAX86051;
XX XX
XX DT 14-SEP-1999 (first entry)
XX DE cDNA encoding human prepro-neuropeptide Y (NPY).
XX KW Human neuropeptide Y; NPY; prepro-neuropeptide Y; mutant;
XX KW serum cholesterol; low density lipoprotein; LDL; ds.
XX XX
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 87..380
XX FT /*tag= a
XX FT sig_peptide 87..170
XX FT /*tag= b
XX FT mutation 106
XX FT /*tag= c
XX FT /*note= "this base is changed to C to encode the mutant
XX FT protein of the invention"
XX PN WO9932518-A1.
XX XX
XX PD 01-JUL-1999.
XX XX
XX PF 16-DEC-1998; 98WO-FI000985.
XX XX
XX PR 19-DEC-1997; 97US-00994946.
XX XX

```


XX (HORM-) HORMOS MEDICAL LTD OY.
 XX Koulu M, Karvonen M, Pesonen U, Uusitupa M;
 XX WPI; 1999-405161/34.
 XX P-PSDB; AAY23828.
 XX
 PT New polynucleotide (I) encoding a prepro-neuropeptide Y (preproNPY).
 XX Claim 2; Fig 1c; 45pp; English.
 XX
 CC The present sequence encodes human prepro-neuropeptide Y (NPY). The
 CC specification describes a polynucleotide encoding a prepro-neuropeptide Y
 CC (preproNPY), where leu (7) is substituted by pro(7). This polynucleotide
 CC is useful for diagnosing and treating humans with a predisposition for
 CC increased serum cholesterol or low density lipoprotein (LDL)
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 SQ

Query Match 98.8%; Score 136.4; DB 2; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60
 DB 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60
 QY 61 CCAGCCAGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120
 DB 61 CCAGCCAGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120
 QY 121 TGACCCCTGCCCTGTGCC 138
 DB 121 TGACCCCTGCCCTGTGCC 138

RESULT 4
 AAC60348
 ID AAC60348 standard; DNA; 551 BP.
 XX AAC60348;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Human neuropeptide Y coding DNA.
 XX
 KW NPY; neuropeptide Y; gene therapy; atherosclerosis; diabetic retinopathy;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200063430-A1.
 XX
 PD 26-OCT-2000.
 XX
 XX 29-MAR-2000; 2000WO-FI000260.
 XX
 PR 15-APR-1999; 99US-00291994.
 XX
 PA (HORM-) HORMOS MEDICAL LTD OY.
 XX
 PI Koulu M, Karvonen M, Pesonen U, Uusitupa M;
 XX WPI; 2000-679606/66.
 XX
 PT Diagnosing diabetic person's susceptibility for developing
 PT atherosclerosis or diabetic retinopathy involves detecting leucine7 to
 PT proline7 polymorphism in signal peptide part of human prepro neuropeptide
 PT Y.
 XX
 PS Disclosure; Fig 1; 4lpp; English.
 XX

CC The present invention relates to diagnosing a diabetic person's
 CC susceptibility for having an increased risk of developing atherosclerosis
 CC or diabetic retinopathy involves determining whether the subject has a
 CC substitution of leucine 7 for proline in the signal peptide part of human
 CC prepro-neuropeptide Y
 XX Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 SQ

Query Match 98.8%; Score 136.4; DB 3; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60
 DB 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGACATAGTACTTGC CGC 60
 QY 61 CCAGCCAGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120
 DB 61 CCAGCCAGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGCTGTCCGAC 120
 QY 121 TGACCCCTGCCCTGTGCC 138
 DB 121 TGACCCCTGCCCTGTGCC 138

RESULT 5
 AAD14527
 ID AAD14527 standard; DNA; 551 BP.
 XX AAD14527;
 AC AAD14527;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human neuropeptide Y (NPY) DNA.
 XX
 KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
 KW FSAD; neutral endopeptidase inhibitor; I:NEP; enkephalinase;
 KW gynaecological; endopeptidase-2; neuropeptide Y; NPY; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT /product= "Human NPY"
 FT sig_peptide 87..170
 FT /*tag= b
 FT mat_peptide 171..278
 FT /*tag= c
 FT /product= "Human mature NPY protein"
 XX
 FN EPI097719-A1.
 XX
 PD 09-MAY-2001.
 XX
 XX 03-NOV-2000; 2000EP-00309722.
 PF
 PR 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.
 PR 12-JUL-2000; 2000GB-00017141.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Maw GN, Wayman CP;
 XX WPI; 2001-309880/33.
 DR P-PSDB; AAE07955.
 XX
 PT Treating females suffering from female sexual dysfunction, preferably
 PT female sexual arousal dysfunction using a neutral endopeptidase inhibitor

PT that potentiates cAMP in female genitalia.
 PS Disclosure; Page 97; 124pp; English.
 XX
 CC The present invention relates to a method for treating female sexual
 CC dysfunction (FSD), preferably female sexual arousal dysfunction (FSAD).
 CC The method comprising using an agent, an inhibitor of neutral
 CC endopeptidase (NEP) EC 3.4.24.11 or I-NEP, which is capable of
 CC potentiating cAMP (which enhances female genital blood flow) in the
 CC sexual genitalia of the females. NEP is also known as enkephalinase or
 CC endopeptidase-2. The agent is optionally admixed with a diluent, carrier
 CC or excipient. The method restores a normal sexual arousal response,
 CC particularly increased blood flow leading to vaginal, clitoral and labial
 CC engorgement. This will result in increased vaginal lubrication via plasma
 CC transduction, increased vaginal compliance and increased genital (e.g.
 CC vaginal and clitoral) sensitivity. The present sequence is human
 CC neurotensin Y (NPY) DNA used in the method of the invention
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 98.8%; Score 136.4; DB 4; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGATAGTACTTGGCCG 60
 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGATAGTACTTGGCCG 60
 QY 61 CCAGCCACGCCCGCGCGCCGAGCCACCATCTAGTAAAGCGACCGGGGCTGTCCGGAC 120
 Db 61 CCAGCCACGCCCGCGCGCGCCGAGCCACCATCTAGTAAAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCTCGCCTGTGCC 138
 Db 121 TGACCTCGCCTGTGCC 138
 RESULT 6
 AAD14517
 ID AAD14517 standard; DNA; 551 BP.
 AC AAD14517;
 XX
 XX 01-NOV-2001 (first entry)
 DE Human neurotensin Y (NPY) DNA.
 KW Human; female sexual dysfunction; FSD; female sexual arousal dysfunction;
 KW FSAD; neurotensin Y; NPY; gynaecological; vasoactive intestinal peptide;
 KW VIP; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT /product= "Human NPY protein"
 FT sig_peptide 87..170
 FT /*tag= b
 FT mat_peptide 171..278
 FT /*tag= c
 FT /product= "Human mature NPY protein"
 XX
 DN EP1097718-A1.
 XX
 XX 09-MAY-2001.
 PD
 PF 03-NOV-2000; 2000EP-00309720.
 XX
 XX 08-NOV-1999; 99GB-00026437.
 PR 18-FEB-2000; 2000GB-00004021.
 PR 26-MAY-2000; 2000GB-00013001.
 PR 05-JUL-2000; 2000GB-00016563.
 PR

PR 12-JUL-2000; 2000GB-00017141.
 XX (PRIZ) PRIZER LTD.
 PA (PFIZ) PRIZER INC.
 XX
 XX Maw GN, Wayman CP;
 PI
 DR WPI: 2001-319199/34.
 DR P-PSDB; AAE07919.
 XX
 XX Treating females suffering from female sexual dysfunction, preferably
 XX female sexual arousal dysfunction using a neurotensin Y inhibitor that
 XX potentiates cAMP in female genitalia.
 XX
 XX Disclosure; Page 129; 165pp; English.
 XX
 CC The patent discloses a method for the treatment of a female suffering
 CC from female sexual dysfunction (FSD), preferably female sexual arousal
 CC dysfunction (FSAD) by the use of an agent which is an inhibitor of
 CC neurotensin Y (NPY). The agent is capable of potentiating cAMP which
 CC enhances female genital (e.g. vaginal or clitoral) blood flow in the
 CC sexual genitalia of the female and is optionally admixed with a diluent
 CC carrier or excipient. The method restores a normal sexual arousal
 CC response namely, increased blood flow leading to vaginal, clitoral and
 CC labial engorgement. This will result in increased vaginal lubrication via
 CC plasma transduction, increased vaginal compliance and increased genital
 CC (e.g. vaginal and clitoral) sensitivity. The method is used for treating
 CC a female suffering from FSD preferably FSAD. The present sequence is a
 CC DNA encoding human neurotensin Y (NPY) protein. NPY exerts an inhibitory
 CC influence over VIP-mediated vasorelaxation and NPY Y1 receptor
 CC antagonists will facilitate the vasorelaxant effect of endogenous
 CC vasoactive intestinal peptide (VIP) released during arousal and enhances
 CC vaginal engorgement
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
 Query Match 98.8%; Score 136.4; DB 4; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGATAGTACTTGGCCG 60
 Db 1 ACCCATCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGACGATAGTACTTGGCCG 60
 QY 61 CCAGCCACGCCCGCGCGCCGAGCCACCATCTAGTAAAGCGACCGGGGCTGTCCGGAC 120
 Db 61 CCAGCCACGCCCGCGCGCGCCGAGCCACCATCTAGTAAAGCGACTGGGGCTGTCCGGAC 120
 QY 121 TGACCTCGCCTGTGCC 138
 Db 121 TGACCTCGCCTGTGCC 138
 RESULT 7
 AAF84086
 ID AAF84086 standard; DNA; 551 BP.
 XX
 XX AAF84086;
 XX
 XX 22-AUG-2001 (first entry)
 DE Human neurotensin Y (NPY) encoding DNA.
 KW Female sexual dysfunction; FSD; female sexual arousal disorder; FSAD;
 KW genital; vaginal; clitoral; blood flow; cAMP; phosphodiesterase; PDE;
 KW CGMP; medicament; human; neurotensin Y; NPY; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT /product= "neurotensin Y"


```
RESULT 9
ABL69726
ID ABL69726 standard; DNA; 551 BP.
XX
AC ABL69726;
XX
DT 15-MAY-2002 (first entry)
XX
DE Prostate cancer related gene sequence SEQ ID NO:8063.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233137P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 8063; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
Query Match 98.8%; Score 136.4; DB 6; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.7e-29;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCCCATCGGTGGTCTCACCCCTCGGAGAGCGTCTGCGCCGACAGCATAGTACTTGCCGC 60
DB 1 ACCCCATCGGTGGTCTCACCCCTCGGAGAGCGTCTGCGCCGACAGCATAGTACTTGCCGC 60
QY 61 CCAGCCAGCCCGCGCGCCGCGCCAGCCATGCTAGGTAAACAGCGCGGGGCTGTCGGAC 120
DB 61 CCAGCCAGCCCGCGCGCGCCGCGCCAGCCATGCTAGGTAAACAGCGCGGGGCTGTCGGAC 120
QY 121 TGACCTCGCCCTGTCCC 138
DB 121 TGACCTCGCCCTGTCCC 138
RESULT 10
ABN84276
ID ABN84276 standard; cDNA; 551 BP.
XX
AC ABN84276;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human neuropeptide Y nucleotide sequence.
XX
KW Neuropeptide Y; NPY; human; inhibitor; male sexual dysfunction;
KW male erectile dysfunction; obesity; anorexia; bulimia; vasotropic;
KW anorectic; therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200247670-A1.
XX
PD 20-JUN-2002.
XX
PF 10-DEC-2001; 2001WO-IB002399.
XX
PR 15-DEC-2000; 2000GB-00030647.
PR 06-APR-2001; 2001GB-00008730.
PR 23-APR-2001; 2001GB-00009910.
PR 04-MAY-2001; 2001GB-00011037.
PR 29-JUN-2001; 2001US-00895367.
PR 13-JUL-2001; 2001US-00905846.
PR 24-AUG-2001; 2001GB-00020679.
XX
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PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 PI Naylor AM, Van Der Graaf PH, Wayman CP;
 XX
 XX WPI; 2002-547828/58.
 DR
 XX
 XX
 XX Use of an inhibitor of neuropeptide Y in the preparation of medicament
 PT for the treatment or prevention of male erectile dysfunction.
 PT
 XX
 XX Disclosure; Fig 4; 179pp; English.
 PS
 XX
 XX The present sequence is a human neuropeptide Y (NPY) polynucleotide
 CC sequence. The invention relates to the use of an inhibitor of NPY, or an
 CC inhibitor of an NPY Y1 receptor, especially an inhibitor selective for an
 CC NPY or NPY Y1 receptor associated with male genitalia, in the preparation
 CC of a medicament for the treatment or prevention of male sexual
 CC dysfunction, especially male erectile dysfunction (MED). A polypeptide
 CC encoded by the present sequence may be used as a target in screens to
 CC identify agents capable of inhibiting NPY. NPY may also be used as a
 CC target to identify agents capable of mediating an increase in
 CC intracavernosal pressure through the inhibition of NPY. The inhibitor
 CC selectively increases intracavernosal pressure of the penis which
 CC facilitates and/or causes penile erection during sexual arousal. In
 CC addition to treatment of MED, the inhibitor can also be used to treat
 CC abnormal drink and food intake disorders, such as obesity, bulimia,
 CC anorexia and metabolic disorders (all claimed)
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 98.8%; Score 136.4; DB 6; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
 Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60

QY 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120
 Db 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTGCC 138
 Db 121 TGACCTCGCCCTGTGCC 138

RESULT 11
 AAL47339
 ID AAL47339 standard; cDNA; 551 BP.
 XX
 AC AAL47339;
 XX
 XX 18-SEP-2002 (first entry)
 DT
 XX Human neuropeptide Y coding sequence.
 DE
 XX Human; neuropeptide Y; NPY; chromosome 7q15.1; SNP; obesity; BMI;
 KW body mass index; single nucleotide polymorphism; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 87..380
 FT /*tag= a
 FT /product= "NPY"
 FT 87..170
 FT sig_peptide /*tag= b
 FT variation replace(106,C)
 FT /*tag= d
 FT 171..380
 FT mat_peptide /*tag= c
 FT
 XX

PN WO200236825-A1.
 XX
 PD 10-MAY-2002.
 XX
 PF 02-NOV-2001; 2001WO-SE002431.
 XX
 PR 03-NOV-2000; 2000SE-00004035.
 XX
 PA (PHAA) PHARMACIA AB.
 XX
 XX Wahlestedt C, Ding B;
 PI
 XX
 XX WPI; 2002-500129/53.
 DR
 DR P-ESDB; AAO18054.
 XX
 XX Diagnosing single nucleotide polymorphism(s) in the human neuropeptide Y
 PT (NPY) gene, useful for diagnosing a predisposition to e.g. obesity, by
 PT determining the nucleic acid sequence at one or more positions of the NPY
 PT gene in the human.
 XX
 XX Example 5; Page 28-29; 37pp; English.
 PS
 XX The present invention relates to a method of diagnosing a predisposition
 CC to obesity in humans by identifying a single nucleotide polymorphism
 CC (SNP) at position 1128 (position 106 of this sequence) of the
 CC neuropeptide Y gene. The gene is found at chromosome 7q15.1. The present
 CC sequence is the NPY coding sequence
 XX
 SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;

Query Match 98.8%; Score 136.4; DB 6; Length 551;
 Best Local Similarity 99.3%; Pred. No. 2.7e-29;
 Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60
 Db 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGC 60

QY 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGCTGTCCGGAC 120
 Db 61 CAGCCACAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACTGGGGCTGTCCGGAC 120

QY 121 TGACCTCGCCCTGTGCC 138
 Db 121 TGACCTCGCCCTGTGCC 138

RESULT 12
 ACF63372
 ID ACF63372 standard; DNA; 551 BP.
 XX
 AC ACF63372;
 XX
 XX 09-OCT-2003 (first entry)
 DT
 XX Human neuropeptide Y gene SEQ ID NO:94.
 DE
 XX
 KW Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquilliser; antiinflammatory; eczema;
 KW antitumor; antimigraine; neuroprotective; antiparkinsonian; analgesic;
 KW gynaecological; virucide; vulnery; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; gene; ds.
 XX
 OS Homo sapiens.

```
XX WO2003006478-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 10-JUL-2002; 2002WO-US021664.
PF
XX
XX 10-JUL-2001; 2001US-0303820P.
PR
XX
XX (OLIG-) OLIGOS ETC INC.
PA
XX
XX Dale RMK, Arrow A, Thompson T;
PI
XX
XX WPI; 2003-221709/21.
DR
XX
XX Composition with a modified oligonucleotide useful for treating a patient
PT with a pathological disorder such as abnormal appetite, hypertension,
PT eczema, anxiety, stress, and cancer.
XX
XX Claim 6; Page 97; 173pp; English.
PS
XX
XX The present invention describes a composition (I) suitable for
CC administration in a mammal, which comprises a modified oligonucleotide
CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
CC modified oligonucleotide is complementary to a region of a gene
CC associated with a pathological disorder. Also described: (1) a
CC nutritional supplement comprising (II); and (2) a cosmetic composition
CC comprising (II), where the modified oligonucleotide is complementary to a
CC region of a gene associated with a skin disorder. (I) and (II) can have
CC hypertensive, antilipemic, vasotropic, dermatological, antidepressant,
CC tranquilizer, antiinflammatory, antitumor, laxative, antimigraine,
CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
CC vulnary, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
CC litholytic activities. (I) can be used for treating a patient with a
CC pathological disorder selected from abnormal appetite, hypertension,
CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant
CC melanoma, and malignant nasal polyps. The nutritional supplement is
CC useful for supplementing the diet of an individual, and the cosmetic
CC composition is useful for improving the appearance of the skin in an
CC individual with a skin disorder. ACF63279 to ACF63410 represent
CC nucleotide sequence given in the exemplification of the present invention
XX
SQ Sequence 551 BP; 131 A; 171 C; 129 G; 120 T; 0 U; 0 Other;
Query Match 98.8%; Score 136.4; DB 7; Length 551;
Best Local Similarity 99.3%; Pred. No. 2.7e-29;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCCATCGCTGGTCTCACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCG 60
DB 1 ACCCATCGCTGGTCTCACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCG 60
QY 61 CCAGCAGCCCGCGCGCCAGCAGCAGCATCTAGGTAAACAGCAGCCGGGCTGTCCGAC 120
DB 61 CCAGCAGCCCGCGCGCCAGCAGCAGCATCTAGGTAAACAGCAGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTCTCC 138
DB 121 TGACCCCTCGCCCTGTCTCC 138
RESULT 13
AAF72746
ID AAF72746 standard; cDNA; 969 BP.
XX
```

```
AC AAF72746;
XX
XX 24-APR-2001 (first entry)
XX
XX Human prostate cancer antigen coding sequence #6.
XX
XX Immunosuppressive; neutropic; neuroprotective; antiviral; vulnary;
KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
KW immune disorder; cardiovascular disorder; neurological disease;
KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
KW antiasthmatic; anticonvulsant; vasotropic; vulnary; human;
KW secreted protein; prostate cancer antigen; ss.
XX
XX Homo sapiens.
XX
XX WO200107476-A1.
XX
XX 01-FEB-2001.
PD
XX
XX 20-JUL-2000; 2000WO-US019666.
PF
XX
XX 21-JUL-1999; 99US-0144972P.
PR
XX 13-AUG-1999; 99US-0148681P.
PR
XX 17-AUG-1999; 99US-0149173P.
PR
XX 06-OCT-1999; 99US-0158004P.
PR
XX 05-APR-2000; 2000US-0194689P.
PR
XX (HUWA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Birse C;
PI
XX WPI; 2001-138554/14.
XX P-PSDB; AAB80278.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
PT antigens, useful for the diagnosis and treatment of disorders such as
PT cancer, leukemia and autoimmune disease.
XX
XX Claim 1; Page 359-360; 433pp; English.
XX
XX The present invention relates to human secreted prostate cancer antigen
CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
CC The coding sequences and proteins of the present invention are useful for
CC preventing, treating or ameliorating a medical condition; and for the
CC diagnosis and treatment of diseases and disorders. Diseases and disorders
CC that can be diagnosed and treated include (auto)immune diseases (e.g.
CC graft versus host disease and rheumatoid arthritis), inflammatory and
CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
CC neurological disorders (e.g. Alzheimer's Parkinson's disease, epilepsy
CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
CC viruses or parasites. They may also be useful for wound healing,
CC epithelial cell proliferation, supporting cell culture, tissue
CC regeneration, birth control and as a food additive or preservative. The
CC coding sequences can be used to generate fusion proteins by linking the
CC coding sequences to the human immunoglobulin G Fc portion coding sequence
CC (AAF72732) for increasing the stability of the fusion protein as compared
CC to the human protein only
XX
SQ Sequence 969 BP; 246 A; 275 C; 225 G; 210 T; 0 U; 13 Other;
Query Match 89.3%; Score 123.2; DB 4; Length 969;
Best Local Similarity 96.2%; Pred. No. 1.5e-25;
Matches 125; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 9 CGCTGGCTCTACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCGCCGCCAC 69
DB 250 CGAGNNCTCTACCCCTCGGAGAGCTGCCCGACAGCATAGTACTTGGCCGCCGCCAC 309
```


CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention

XX
 SQ Sequence 599 BP; 163 A; 169 C; 139 G; 120 T; 0 U; 8 Other;

Query Match 79.3%; Score 109.4; DB 3; Length 599;
 Best Local Similarity 98.4%; Pred. No. 1.2e-21;
 Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGCCTCGCCCGACGCGCGCG 75

Db 14 TCTCACCCTCGGAGACGCTCGCCCGACAGCATAGTACTTGCCTCGCCCGACGCGCGCG 73

Qy 76 CGCCAGCCACCATGCTAGGTAAACAGCGACCGGGGCTGTCCGGACTGACCTCGCCCTGT 135

Db 74 CGCCA-CCACCATGCTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCTCGCCCTGT 132

Qy 136 CCC 138

Db 133 CCC 135

Search completed: April 26, 2004, 14:04:43
 Job time : 272 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 2161 Seconds
(without alignments)
1906.979 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

Sequence: 1 accccatccgctgctctca.....actgacctcgccctgtccc 138

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_estl.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gssl.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136.4	98.8	463	14	CA772698
2	136.4	98.8	584	12	BI457963
3	136.4	98.8	873	13	BU930481
4	135.4	98.1	300	9	AU100303

5	133.4	96.7	136	9	AU077324
6	126.4	91.6	521	9	AI879081
7	125.4	90.9	556	13	BQ721485
8	125.4	90.9	557	13	BQ925183
9	125.4	90.9	963	13	BQ876913
c 10	124.8	90.4	550	9	AI928896
c 11	123.8	89.7	544	9	AI826374
12	123.4	89.4	468	13	AI101548
13	122.4	88.7	433	9	AI929147
14	112.4	81.4	567	13	BQ932266
15	105.2	76.2	1123	13	BQ886097
16	87	63.0	766	13	BQ930120
17	85	61.6	1695	10	BF680552
c 18	78.4	56.8	498	9	AI199681
19	69.4	50.3	424	9	AA061961
20	69.4	50.3	443	9	AI385504
21	69.4	50.3	492	13	BX527459
22	69.4	50.3	556	11	AK002982
23	69.4	50.3	585	13	BU937569
24	69.4	50.3	591	13	BU558492
25	69.4	50.3	600	13	BU604192
26	69.4	50.3	926	13	BU936355
27	68	49.3	489	10	BE653691
28	68	49.3	493	13	BQ084972
c 29	68	49.3	534	13	BQ084688
30	68	49.3	569	13	BQ564644
c 31	66.8	48.4	574	9	AI198311
32	64.6	46.8	435	14	CB792893
33	61.6	44.6	402	14	CB769232
34	61.6	44.6	520	12	BG664369
35	61.6	44.6	529	14	CB719328
36	61.6	44.6	544	14	CB612099
c 37	61.6	44.6	587	14	CB585333
38	61.4	44.5	408	9	AA270394
39	61.4	44.5	483	14	W70782
40	60.6	43.9	570	12	BQ044605
41	60	43.5	364	13	BQ290146
42	55	39.9	454	14	CB741987
43	55	39.9	461	14	CB736748
44	55	39.9	499	14	CB712314
45	55	39.9	500	14	CB712006

ALIGNMENTS

RESULT 1

CA772698

LOCUS

DEFINITION

CA772698 463 bp mRNA linear EST 03-DEC-2002

1083901.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6133056 5',

similar to SW:NEUY_HUMAN P01303 NEUROPEPTIDE Y PRECURSOR ; , mRNA

sequence.

CA772698

CA772698.1 GI:26009965

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

REFERENCE

1 (bases 1 to 463)

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Iemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blstein,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,

Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,

Williams,T., Jackson,X. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: i083901.xl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmeitton@biohph.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

Putative full length read

vector to vector length is 598

Seq primer: -40RP from Gibco.

FEATURES

source

Location/Qualifiers
1. 463
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:6133056"
/tissue type="Purified pancreatic islet"
/lab host="DH10B"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming. ~1kb. 5'
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 98.8%; Score 136.4; DB 14; Length 463;
Best Local Similarity 99.3%; Pred. No. 2.9e-23;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTGCGCGACAGCATAGTACTTGCGCG 60
|||||
Db 28 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTGCGCGCGACAGCATAGTACTTGCGCG 87
|||||

QY 61 CCAGCCACGCCCGCGCGCGAGCACCATCTAGGTAAACAAGCGACGGGGCTGTCGGGAC 120
Db 89 CCAGCCACGCCCGCGCGCGAGCACCATCTAGGTAAACAAGCGACTGGGGCTGTCGGGAC 147
|||||

QY 121 TGACCTCGCCCTGTGCC 138
Db 148 TGACCTCGCCCTGTGCC 165
|||||

RESULT 2
BI457963
LOCUS
DEFINITION
603198956F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5278692 5',
mRNA sequence.
ACCESSION
BI457963
VERSION
BI457963.1 GI:15248619
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov
Plate: LLAM11703 row: o column: 13
High quality sequence stop: 584.

FEATURES

source

Location/Qualifiers
1. 584
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5278692"
/tissue type="hypothalamus"
/lab host="DH10B"
/clone lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-ATTCTTTTCTTTT-3', size-selected for average
insert size 2.3 kb and normalized to 80T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 98.8%; Score 136.4; DB 12; Length 584;
Best Local Similarity 99.3%; Pred. No. 3.1e-23;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTGCGCGACAGCATAGTACTTGCGCG 60
|||||
Db 8 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTGCGCGCGACAGCATAGTACTTGCGCG 67
|||||

QY 61 CCAGCCACGCCCGCGCGCGAGCACCATCTAGGTAAACAAGCGACGGGGCTGTCGGGAC 120
Db 68 CCAGCCACGCCCGCGCGCGAGCACCATCTAGGTAAACAAGCGACTGGGGCTGTCGGGAC 127
|||||

QY 121 TGACCTCGCCCTGTGCC 138
Db 128 TGACCTCGCCCTGTGCC 145
|||||

RESULT 3
BU930481
LOCUS
DEFINITION
AGENCOURT 10424773 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668512
5', mRNA sequence.
ACCESSION
BU930481
VERSION
BU930481.1 GI:24119300
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov
Plate: LLM2942 row: 1 column: 16
High quality sequence stop: 510.

FEATURES

source

Location/Qualifiers
1. 873
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```

/clone="IMAGE:6668512"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
(ggccattagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGGCGGCGGCGGCAGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

ORIGIN

```

Query Match      99.8%; Score 136.4; DB 13; Length 873;
Best Local Similarity 99.3%; Pred. No. 3.4e-23;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGC 60
Db 4 ACCCATCCGCTGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGC 63
QY 61 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120
Db 64 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 123
QY 121 TGACCTTCGCCCTGTCCC 138
Db 124 TGACCTTCGCCCTGTCCC 141
```

RESULT 4

```

AU100303
LOCUS              300 bp mRNA linear EST 05-APR-2001
DEFINITION        Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
Zrv6c665 similar to Human neuro peptide Y (NPY) mRNA, mRNA sequence.
ACCESSION         AU100303
VERSION           AU100303.1 GI:13551432
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE         1 (bases 1 to 300)
AUTHORS           Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S.,
Okubo, K., Suyama, A. and Sugano, S.
In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
```

TITLE

```

This clone was obtained from a '5'-end-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
Location/Qualifiers
1. .136
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Zrv6c665"
/clone_lib="Sugano cDNA library"
```

FEATURES

```

source
1. .136
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Zrv6c665"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      98.1%; Score 135.4; DB 9; Length 300;
Best Local Similarity 98.6%; Pred. No. 4.6e-23;
```

```

Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGC 60
Db 1 ACCCATCCGCTGCTCTCACCCCTCGANACGCTCGCCGACAGCATAGTACTTGC 60
QY 61 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCTTCGCCCTGTCCC 138
Db 121 TGACCTTCGCCCTGTCCC 138
```

RESULT 5

```

AU077324
LOCUS              136 bp mRNA linear EST 04-MAY-2000
DEFINITION        Sugano cDNA library Homo sapiens cDNA clone Zrv6c665
similar to 5'-end region of Human neuro peptide Y (NPY) mRNA, mRNA
sequence.
ACCESSION         AU077324
VERSION           AU077324.1 GI:7440000
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE         1 (bases 1 to 136)
AUTHORS           Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H.,
Tsunoda, T., Watanabe, M., Komatsu, T., Ota, T., Isogai, T., Suyama, A.
and Sugano, S.
Statistical analysis of the 5' untranslated region of human mRNA
using 'Oligo-Capped' cDNA libraries
Genomics 64 (3), 286-297 (2000)
20221373
PUBMED            10756096
COMMENT           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
```

FEATURES

```

source
1. .136
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Zrv6c665"
/clone_lib="Sugano cDNA library"

ORIGIN
Query Match      96.7%; Score 133.4; DB 9; Length 136;
Best Local Similarity 98.5%; Pred. No. 1.2e-22;
Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGCTCTCACCCCTCGAGACGCTCGCCGACAGCATAGTACTTGC 60
Db 1 ACCCATCCGCTGCTCTCACCCCTCGANACGCTCGCCGACAGCATAGTACTTGC 60
QY 61 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120
Db 61 CCAGCCACGCGCGCGCGCCAGCACCATGCTAGTAAACAGCGACTGGGCTGTCCGGAC 120
QY 121 TGACCTTCGCCCTGTGC 136
Db 121 TGACCTTCGCCCTGTGC 136
```

```

RESULT 6
AI879081      521 bp      mRNA      linear      EST 23-AUG-1999
LOCUS      aus4b11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
DEFINITION      IMAGE:2518557 5', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION      AI879081      GI:5553130
VERSION      AI879081.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 521)
AUTHORS      Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., McCabe, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE      WashU-NCI human EST Project
JOURNAL      Unpublished (1997)
COMMENT      Other ESTs: aus4b11.x1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
FEATURES             source
    location/Qualifiers
        1..521
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2518557"
        /sex="male"
        /tissue_type="frontal lobe"
        /dev_stage="5 months post-conception"
        /lab_host="DH10B"
        /clone_lib="Schneider fetal brain 00004"
        /note="Organ: brain; Vector: pBluescript SK (Stratagene);
        Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
        prepared from human fetal brain tissue. 5' and 3'
        adaptors were used in cloning as follows: 5' adaptor
        sequence:
        5'-GAGAGAGAGAGAGCTCAAGGATCTTAAATAATTAATCCCGCCCGCC-3',
        and 3' adaptor sequence:
        5'-GAGAGAGAGAGCTCGAGTTTCTTTTCTTTT-3'. The library was
        size-selected for >0.5 kb inserts and has an average
        insert size estimated at 1.2 kb. This library was
        constructed using the CAP-trapper method for full-length
        enrichment and has not undergone amplification. Library
        was constructed by Dr. Claudio Schneider (INCI-AREA
        Science Park, Trieste, Italy)."
ORIGIN
Query Match      91.6%; Score 126.4; DB 9; Length 521;
Best Local Similarity 99.2%; Pred. No. 8.1e-21;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      11      CTGGCTCTACCCCTCGGAGCGCTCGCCGACAGATAGTACTTCCGCCCGCCAGCCG 70
Db      1      CTGGCTCTACCCCTCGGAGCGCTCGCCGACAGATAGTACTTCCGCCCGCCAGCCG 60
QY      71      CGCGCGCGCCAGCCACCATCTAGGTAAACAAGGACCGGGGCTGTCCGGACTGACCTCGC 130
Db      61      CGCGCGCGCCAGCCACCATCTAGGTAAACAAGGACCTGGGGCTGTCCGGACTGACCTCGC 120
QY      131      CTTGTCCC 138

```

Db 121 CTTGTCCC 128

RESULT 7
BQ721485
LOCUS
DEFINITION
AGENCOURT 8234409 Lupski sy pathetic_trunk Homo sapiens cDNA clone
IMAGE:6188546 5', mRNA sequence.
ACCESSION
BQ721485
VERSION
BQ721485.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 556)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1584 row: f column: 03
High quality sequence stop: 555.
Location/Qualifiers
1..556
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6188546"
/sex="male"
/tissue_type="sy pathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski sy pathetic trunk"
/note="Vector: pCMV-SPORT6 (life technologies); Site 1:
NotI; Site 2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCGC-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

QY 12 TGCTCTACCCCTCGGAGCGCTCGCCGACAGATAGTACTTCCGCCCGCCAGCCG 71

Db 1 TGCTCTACCCCTCGGAGCGCTCGCCGACAGATAGTACTTCCGCCCGCCAGCCG 60

QY 72 CGCGCGCGCCAGCCACCATCTAGGTAAACAAGGACCGGGGCTGTCCGGACTGACCTCGC 131

Db 61 CGCGCGCGCCAGCCACCATCTAGGTAAACAAGGACCTGGGGCTGTCCGGACTGACCTCGC 120

QY 132 CTTGTCCC 138

Db 121 CTTGTCCC 127

RESULT 8
BQ25183

LOCUS BQ925183 557 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT 8821446 Lupski_sciatic nerve Homo sapiens cDNA clone
IMAGE:6203754 5', mRNA sequence.
ACCESSION BQ925183
VERSION BQ925183.1 GI:22340214
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 557)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM13623 row: o column: 19
 High quality sequence stop: 556.
FEATURES Location/Qualifiers
 source
 1..557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6203754"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sciatic nerve"
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACCGCTCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGCTGGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
ORIGIN
 Query Match 90.9%; Score 125.4; DB 13; Length 557;
 Best Local Similarity 99.2%; Pred. No. 1.4e-20;
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 71
 Db 1 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 60
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120
 QY 132 CTGTCCC 138
 Db 121 CTGTCCC 127
RESULT 10
LOCUS BQ876913 963 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT 8417678 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6193004 5', mRNA sequence.
ACCESSION BQ876913
VERSION BQ876913.1 GI:22268921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM13623 row: o column: 19
 High quality sequence stop: 556.
FEATURES Location/Qualifiers
 source
 1..557
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6203754"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sciatic nerve"
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACCGCTCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGCTGGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
ORIGIN
 Query Match 90.9%; Score 125.4; DB 13; Length 557;
 Best Local Similarity 99.2%; Pred. No. 1.4e-20;
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 71
 Db 1 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 60
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120
 QY 132 CTGTCCC 138
 Db 121 CTGTCCC 127
RESULT 9
LOCUS BQ876913 963 bp mRNA linear EST 23-AUG-1999
DEFINITION au65f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
 (HUMAN); mRNA sequence.
ACCESSION AI928896
VERSION AI928896.1 GI:5664860
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 550)

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM13595 row: o column: 21
 High quality sequence stop: 517.
FEATURES Location/Qualifiers
 source
 1..963
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6193004"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sympathetic trunk"
 /notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACCGCTCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGCTGGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."
ORIGIN
 Query Match 90.9%; Score 125.4; DB 13; Length 963;
 Best Local Similarity 99.2%; Pred. No. 1.6e-20;
 Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 71
 Db 1 TGGCTCTACCCCTCGGAGCGCTCGCCGACGATAGTACTTGGCGCCACGCCAGCC 60
 QY 72 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCGGACTGACCCCTGCC 131
 Db 61 CGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCGGACTGACCCCTGCC 120
 QY 132 CTGTCCC 138
 Db 121 CTGTCCC 127
RESULT 10
LOCUS AI928896/c 550 bp mRNA linear EST 23-AUG-1999
DEFINITION au65f07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519653 3', similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
 (HUMAN); mRNA sequence.
ACCESSION AI928896
VERSION AI928896.1 GI:5664860
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 550)

AUTHORS
Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, F., Wyllie, F., Waterston, R. and Wilson, R.
WASHU-NCI human EST project
Unpublished (1997)
JOURNAL
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 481.

FEATURES
source
1..550
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519653"
/sex="male"
/tissue type="frontal lobe"
/dev stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SST1; Site 2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-GAGAGAGAGAGAGCTCAGGATCCTTAATTAATTAATCCCGCCCGCC-3' and 3' adaptor sequence:
5'-GAGAGAGAGAGCTCAGGATCCTTAATTAATTAATCCCGCCCGCC-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy)."

REFERENCE
1 (bases 1 to 544)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 490 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 461.

FEATURES
source
1..544
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2418310"
/sex="male"
/tissue type="normal prostate"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr22"
/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 89.7%; Score 123.8; DB 9; Length 544;
Best Local Similarity 98.4%; Pred. No. 3.5e-20;
Matches 125; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 TGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCGCGCCGACGCGCC 71
Db 544 TGGCTCTCACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTCGCGCCGACGCGCC 485
QY 72 CGCGCGCGAGCCACCATGCTAGGTAAACAGCGCGGCGCTCTCGGACTGACCTCGCC 131
Db 484 CGCGCGCGAGCCACCATGCTAGGTAAACAGCGGCTCTCGGACTGACCTCGCC 425
QY 132 CTGTGCC 138
Db 424 CTGTGCC 418

RESULT 12
BX101548 468 bp mRNA linear EST 06-FEB-2003
LOCUS BX101548 Soares placenta 8to9weeks 2NdbP8to9W Homo sapiens CDNA
DEFINITION clone IMAGE:998K074642; IMAGE:1894398, mRNA sequence.
ACCESSION BX101548
VERSION BX101548.1 GI:278444953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 468)
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, B., Peters, M., Radelof, U., Schneider, D. and Korn, B.
HUMAN UNIGENESet - RZPD3
Unpublished (2003)
CONTACT: Ina Rolfes

ORIGIN
Query Match 90.4%; Score 124.8; DB 9; Length 550;
Best Local Similarity 96.9%; Pred. No. 2e-20;
Matches 126; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 9 CGCTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGAGCCAC 68
Db 550 CGNTGGCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGAGCCAC 491
QY 69 GCGCGCGCGAGCCACCATGCTAGGTAAACAGCGGCGCTCTCGGACTGACCTTC 128
Db 490 GCGCGCGCGAGCCACCATGCTAGGTAAACAGCGGCTCTCGGACTGACCTTC 431
QY 129 GCCCTGTGCC 138
Db 430 GCCCTGTGCC 421

RESULT 11
AI826374/c 544 bp mRNA linear EST 07-MAR-2000
LOCUS wk44g12.x1 NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:2418310 3'
DEFINITION similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AI826374
VERSION AI826374.1 GI:5447045
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998K074642.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rofls
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGAAACAGCTATGAC.

FEATURES

source

1. .468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998K074642 ; IMAGE:1894398"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_Placenta 8to9weeks 2NBP8to9W"
/note="Organ: Placenta; Vector: p77r3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGATTTTATTTTATTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77r3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN

Query Match 89.48; Score 123.4; DB 13; Length 468;
Best Local Similarity 99.28; Pred. No. 4.2e-20;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 GCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACGACGCGCG 73
|||||
Db 1 GCTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACGACGCGCG 60
QY 74 CGGCCGACGACCATGTAGTAAACAGCGACGCGGCTGTCCGACTGACCCCTGCGCCT 133
|||||
Db 61 CGGCCGACGACCATGTAGTAAACAGCGACTGGGCTGTCCGACTGACCCCTGCGCCT 120
QY 134 GTCCC 138
|||||
Db 121 GTCCC 125

RESULT 13

AI929147

LOCUS

AI929147 433 bp mRNA linear EST 23-AUG-1999
au65f07.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519653 5' similar to gb:K01911 NEUROPEPTIDE Y PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION

AI929147

VERSION

AI929147.1

GI:5665111

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 433)

Haller L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,

Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,

Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,

Theising B., White Y., Wylie T., Waterston R. and Wilson R.

WashU-NCI human EST Project

Unpublished (1997)

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco.

FEATURES

source

1. .433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2519653"
/sex="male"
/tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
/clone_lib="Schneider fetal brain 00004"
/note="Organ: brain; Vector: pBluescript SK (Stratagene);
Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was
prepared from human fetal brain tissue. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence:
5'-GAGAGAGAGAGAGCTCAAGGATCTTTAATTAAATCCCGCCCCCCC-3'
and 3' adaptor sequence:
5'-GAGAGAGAGAGCTGAGTTTATTTTATTTT-3'. The library was
size-selected for >0.5 kb inserts and has an average
insert size estimated at 1.2 kb. This library was
constructed using the CAP-trapper method for full-length
enrichment and has not undergone amplification. Library
was constructed by Dr. Claudio Schneider (LNCIB-Area
Science Park, Trieste, Italy)."

ORIGIN

Query Match 88.78; Score 122.4; DB 9; Length 433;
Best Local Similarity 99.24; Pred. No. 7.3e-20;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACGACGCGCG 74
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Db 1 CTCTACCCCTCGGAGACGCTCGCCGACAGCATAGTACTTGGCGCCGACGACGCGCG 60
QY 75 GCGCCGACGACCATGTAGTAAACAGCGACGCGGCTGTCCGACTGACCCCTGCGCCTG 134
|||||
Db 61 GCGCCGACGACCATGTAGTAAACAGCGACTGGGCTGTCCGACTGACCCCTGCGCCTG 120
QY 135 TCCC 138
|||||
Db 121 TCCC 124

RESULT 14

BQ932266

LOCUS

BQ932266 567 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8804926 Lupeki sciatic nerve Homo sapiens cDNA clone
IMAGE:6197017 5', mRNA sequence.

ACCESSION

BQ932266

VERSION

BQ932266.1

GI:22347297

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 567)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13606 row: g column: 02
 High quality sequence stop: 566.

FEATURES

Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6197017"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sciatic nerve"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGGCTCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

ORIGIN

Query Match 81.4%; Score 112.4; DB 13; Length 567;
 Best Local Similarity 99.1%; Pred. No. 2.1e-17;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 25 TCGGAGACGTCGCCCGCAGCATAGTACTTCCGCCCGCAGCACGCCCGCGCCAGCCA 84
 Db 1 TCGGAGACGTCGCCCGCAGCATAGTACTTCCGCCCGCAGCACGCCCGCGCCAGCCA 60
 QY 85 CCATCTAGGTAAACAGCGCGGCTGTCGGAGTACCTCGCCCTGTCCTCC 138
 Db 61 CCATCTAGGTAAACAGCGCTGGGGCTGTCCGGACTGACCTCGCCCTGTCCTCC 114

RESULT 15

BQ886097 1123 bp mRNA linear EST 16-AUG-2002
 AGENCOURT_8673508 Lupski_sciatic_nerve Homo sapiens cDNA clone
 IMAGE:6199943 5', mRNA sequence.
 BQ886097
 BQ886097.1 GI:22278111
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1123)
 NIH-MGC <http://mgi.mcg.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13613 row: p column: 24
 High quality sequence start: 90
 High quality sequence stop: 266.
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 1..1123

FEATURES

Location/Qualifiers
 1..1123

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6199943"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sciatic nerve"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGGCTCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.87 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

ORIGIN

Query Match 76.2%; Score 105.2; DB 13; Length 1123;
 Best Local Similarity 89.9%; Pred. No. 1.4e-15;
 Matches 124; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
 QY 1 ACCCCATCCGCTGGCTCTCACCCCTCGGAGACGCTCGCCCGCAGCATAGTACTTCCGCG 60
 Db 41 ACCGCCACGCGTCCGCTCACCCCTCGGAGACGCTCGCCCGCAGCATAGTACTCGACGC 99
 QY 61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGCGCGGCTGTCCGGAC 120
 Db 100 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGAGTGGGGCTGTCCGGAC 159
 QY 121 TGACCCCTCGCCCTGTCCC 138
 Db 160 TGACCCCTCGCCCTGTCCC 177

Search completed: April 26, 2004, 15:45:52
 Job time : 2161 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 13:55:21 ; Search time 59.5 Seconds
(without alignments)
1287.113 Million cell updates/sec

Title: US-09-645-590-2

Perfect score: 138

Sequence: 1 accccatcgctggctctca.....actgacctgcctgtccc 138

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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2: /cgn2_6/prodata/2/ina/5B COMB seq.*

3: /cgn2_6/prodata/2/ina/6A COMB seq.*

4: /cgn2_6/prodata/2/ina/6B COMB seq.*

5: /cgn2_6/prodata/2/ina/PCTUS COMB seq.*

6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	1588	4	US-09-976-594-625
2	136.4	98.8	551	3	US-08-994-946A-5
3	136.4	98.8	551	4	US-09-291-994-5
4	111.6	80.9	122	4	US-09-621-976-8234
5	89.4	64.8	325	3	US-08-994-946A-1
6	89.4	64.8	325	4	US-09-291-994-1
7	50.4	36.5	247	3	US-08-994-946A-2
8	50.4	36.5	247	4	US-09-291-994-2
9	32.2	23.3	945	4	US-09-252-991A-14797
10	32.2	23.3	2550	4	US-09-252-991A-14954
11	31.8	23.0	1242	4	US-09-252-991A-9668
12	31.8	23.0	1521	4	US-09-252-991A-9746
13	31.8	23.0	2511	4	US-09-252-991A-9494
14	31.8	23.0	2583	4	US-09-252-991A-9541
15	31.2	22.6	999	4	US-09-252-991A-14871
16	31.2	22.6	1608	4	US-09-252-991A-14871
17	30.8	22.3	1108	4	US-09-800-729-42
18	30.8	22.3	1141	4	US-09-800-729-78
19	30.8	22.3	1297	4	US-09-800-729-80
20	30.2	21.9	1518	4	US-09-489-039A-6357
21	30	21.7	1546	4	US-09-383-318A-1
22	29.6	21.4	480	4	US-09-674-608A-4
23	29.2	21.2	576	4	US-09-252-991A-7331
24	29.2	21.2	670	4	US-09-009-816-3
25	29.2	21.2	1104	4	US-09-009-816-1
26	29.2	21.2	1302	4	US-09-252-991A-7221
27	29.2	21.2	1551	4	US-09-252-991A-7473

28	29.2	21.2	1578	4	US-09-252-991A-7410	Sequence 7410, Ap
c 29	29	21.0	411	4	US-09-252-991A-8321	Sequence 8321, Ap
30	29	21.0	783	4	US-09-252-991A-8452	Sequence 8452, Ap
c 31	29	21.0	966	4	US-09-252-991A-8354	Sequence 8354, Ap
c 32	29	21.0	1110	4	US-09-252-991A-8388	Sequence 8388, Ap
c 33	29	21.0	1131	4	US-09-252-991A-8486	Sequence 8486, Ap
c 34	29	21.0	3638	4	US-09-369-364A-8	Sequence 8, Appli
c 35	28.8	20.9	807	4	US-09-489-039A-5230	Sequence 5230, Ap
c 36	28.6	20.7	804	4	US-09-252-991A-15809	Sequence 15809, A
c 37	28.6	20.7	2073	4	US-09-252-991A-15779	Sequence 15779, A
c 38	28.6	20.7	3664	1	US-07-880-913-1	Sequence 1, Appli
c 39	28.4	20.6	279	4	US-09-252-991A-8120	Sequence 8120, Ap
40	28.4	20.6	735	4	US-09-252-991A-8185	Sequence 8185, Ap
41	28.4	20.6	1247	1	US-08-278-729A-32	Sequence 32, Appl
42	28.4	20.6	1247	1	US-08-155-343A-32	Sequence 32, Appl
43	28.4	20.6	1247	1	US-08-406-672-32	Sequence 32, Appl
44	28.4	20.6	1247	1	US-08-643-563A-32	Sequence 32, Appl
45	28.4	20.6	1247	1	US-08-643-763A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-976-594-625
; Sequence 625, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 625
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1344185CB1
; NAME/KEY: unsure
; LOCATION: 7, 19, 25, 32, 45, 59, 88, 96, 108, 116, 124, 150, 167, 181, 191, 216,
; LOCATION: 221, 226, 233, 246, 264, 276, 286, 303, 307, 315, 330, 332, 336, 351, 359,
; LOCATION: 363, 373, 377, 382, 395, 407, 424, 431, 435, 442, 446, 470, 488, 492, 499,
; LOCATION: 504, 537, 551, 556, 583, 592, 596, 604, 615, 641, 671, 696, 709, 714, 726,
; LOCATION: 738, 747, 751, 756, 762, 774, 810, 842, 844, 906
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-625

Query Match 100.0%; Score 138; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 1.5e-31;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTAGTATCTTCCCGC 60
DB	1031	ACCCATCGCTGGCTCTCACCCCTCGGAGAGCTCGCCGACGATAGTAGTATCTTCCCGC 1090
QY	61	CCAGCCAGCCCGCGCCGACGATCTAGTAAAGCGACCGGGGCTGTCCGGAC 120
DB	1091	CCAGCCAGCCCGCGCCGACGATCTAGTAAAGCGACCGGGGCTGTCCGGAC 1150
QY	121	TGACCCCTGCCCTGTCCC 138
DB	1151	TGACCCCTGCCCTGTCCC 1168

RESULT 2
US-08-994-946A-5

; Sequence 5, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,946A
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihmen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 87..170
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..377
; US-08-994-946A-5

Query Match 98.8%; Score 136.4; DB 3; Length 551;
Best Local Similarity 99.3%; Pred. No. 3.8e-31;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 CCAGCCACGCCCGCGCGCCAGCCATCTAGGTAAACAAGCGACCGGGGCTGTCGGGAC 120
QY 121 TGACCTCGCCCTGTCCC 138
DB 121 TGACCTCGCCCTGTCCC 138

RESULT 3

US-09-291-994-5
; Sequence 5, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti

; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; TITLE OF INVENTION: Y Gene.
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)..(377)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (87)..(170)
; US-09-291-994-5

Query Match 98.8%; Score 136.4; DB 4; Length 551;
Best Local Similarity 99.3%; Pred. No. 3.8e-31;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGTCCGCGACAGCATAGTACTTGCCGC 60
QY 61 CCAGCCACGCCCGCGCGCCAGCCATCTAGGTAAACAAGCGACCGGGGCTGTCGGGAC 120
DB 61 CCAGCCACGCCCGCGCGCCAGCCATCTAGGTAAACAAGCGACCGGGGCTGTCGGGAC 120
QY 121 TGACCTCGCCCTGTCCC 138
DB 121 TGACCTCGCCCTGTCCC 138

RESULT 4

US-09-621-976-8234
; Sequence 8234, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8234
; LENGTH: 122
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-8234

Query Match 80.9%; Score 111.6; DB 4; Length 122;
Best Local Similarity 93.4%; Pred. No. 5.3e-24;
Matches 114; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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DB 1 ACCCATCGCTGGCTCTCACCCCTCGGAGAGCGTCCGCGACAGCATAGTACTTGCCGC 60
QY 61 CCAGCCACGCCCGCGCGCCAGCCATCTAGGTAAACAAGCGACCGGGGCTGTCGGGAC 120
DB 61 CCAGCCACGCCCGCGCGCCAGCCATCTAGGTAAACAAGCGACCGGGGCTGTCGGGAC 120
QY 121 TG 122

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Db      121 TG 122
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;
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-291-994-1

Query Match      64.8%; Score 89.4; DB 4; Length 325;
Best Local Similarity 89.7%; Pred. No. 1.7e-17;
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCGCCGAGCATAGTACTTGGCGC 60
      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCGCCGAGCATAGTACTTGGCGC 269

Db      61 CCAGCCACGCGCCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
      270 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAGTCTAGACCCCGTCTG 316

QY      61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
      270 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAGTCTAGACCCCGTCTG 316

Db      61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
      270 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAGTCTAGACCCCGTCTG 316

RESULT 7
US-08-994-946A-2
; Sequence 1, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 13th Street NW, Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,946A
; FILING DATE: 19-DEC-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2328-110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-994-946A-1

Query Match      64.8%; Score 89.4; DB 3; Length 325;
Best Local Similarity 89.7%; Pred. No. 1.7e-17;
Matches 96; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      1 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCGCCGAGCATAGTACTTGGCGC 60
      210 ACCCATCCGCTGGCTCTCACCCCTCGGAGACGCTGCGCCGAGCATAGTACTTGGCGC 269

Db      61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
      270 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAGTCTAGACCCCGTCTG 316

QY      61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
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Db      61 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAAACAGCGACCG 107
      270 CCAGCCACGCGCGCGCGCCAGCCACCATGCTAGGTAGTCTAGACCCCGTCTG 316

RESULT 6
US-09-291-994-1
; Sequence 1, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
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Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 87 ATGCTAGTAAACAGCGACCGGGCTGTCGGAGTACCCCTGCGCTGTCCC 138
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCCCTGCGCTGTCCC 81

RESULT 8

US-09-291-994-2

; Sequence 2, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulou, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; TITLE OF INVENTION: Y Gene.
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291,994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-994-2

Query Match 36.5%; Score 50.4; DB 4; Length 247;
Best Local Similarity 98.1%; Pred. No. 3.7e-06;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 ATGCTAGTAAACAGCGACCGGGCTGTCGGAGTACCCCTGCGCTGTCCC 138
Db 30 ATGCTAGTAAACAGCGACTGGGCTGTCCGAGTACCCCTGCGCTGTCCC 81

RESULT 9

US-09-252-991A-14797/c

; Sequence 14797, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14797
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14797

Query Match 23.3%; Score 32.2; DB 4; Length 945;
Best Local Similarity 52.6%; Pred. No. 0.84;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTGCGCCGACAGCATAGTACTTGGCGC 60
Db 611 ACCCGCGGGTGGCAACCGAGACGTTGACATCGCCCGCTGCCCTGCCCGCAGCATC 552
QY 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGTGTCCGGAC 120
Db 551 CCCGCGAGCGCGCTCGGCAACACCAAGGTGGGACAGCAACGCGGAGCTCGGCC 492

QY 121 TGACCCCTCGCCCT 133
Db 491 TCAATCTCGTCT 479

RESULT 10

US-09-252-991A-14954

; Sequence 14954, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14954
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14954

Query Match 23.3%; Score 32.2; DB 4; Length 2550;
Best Local Similarity 52.6%; Pred. No. 0.94;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTCACCCCTCGGAGAGCTGCGCCGACAGCATAGTACTTGGCGC 60
Db 1880 ACCCGCGGGTGGCAACCGAGACGTTGACATCGCCCGCTGCCCTGCCCGCAGCATC 1939
QY 61 CCAGCCAGCGCGCGCGCCAGCCACCATGCTAGGTAAACAAGCGACCGGGGTGTCCGGAC 120
Db 1940 CCCGCGAGCGCGCTCGGCAACACCAAGGTGGGACAGCAACGCGGAGCTCGGCC 1999

QY 121 TGACCCCTCGCCCT 133
Db 2000 TCAATCTCGTCT 2012

RESULT 11

US-09-252-991A-9668/c

; Sequence 9668, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9668
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9668

Query Match 23.0%; Score 31.8; DB 4; Length 1242;
Best Local Similarity 54.8%; Pred. No. 1.1;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 24 CTCGGAGAGCTGCCCGCAGCAGCATAGTACTTGGCGCCAGCCAGCGCGCGCGCAGCC 83

Db 947 CTCGAAGACCGCCAGACCGCTCTCGATATGGCCAGCGCCGCGGACGCTTCCTGGCC 888
QY 84 ACCATCTAGGTAAACAGCGACCGGGCTGTCGGAGCTGACCTCGCCCTGTGCC 138
Db 887 AACATGAGCCAGAGATCCGACGCGCTGAACGGCTGCTCGGCATGCTCTCGC 833

RESULT 12

US-09-252-991A-9746/c
; Sequence 9746, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9746
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9746

Query Match 23.0%; Score 31.8; DB 4; Length 1521;
Best Local Similarity 54.8%; Pred. No. 1.2;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 24 CTCGGAGAGCTCGCCGACAGCATAGTACTTCCGCCAGCCAGCCGCGCGCCAGCC 83
Db 1506 CTCGAAGACCGCCGACAGCGCTCTCGATATGGCCAGCGCCGCGGACGCTTCCTGGCC 1447
QY 84 ACCATCTAGGTAAACAGCGACCGGGCTGTCGGAGCTGACCTCGCCCTGTGCC 138
Db 1446 AACATGAGCCAGAGATCCGACGCGCTGAACGGCTGCTCGGCATGCTCTCGC 1392

RESULT 13

US-09-252-991A-9494
; Sequence 9494, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9494
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9494

Query Match 23.0%; Score 31.8; DB 4; Length 2511;
Best Local Similarity 54.8%; Pred. No. 1.2;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 24 CTCGGAGAGCTCGCCGACAGCATAGTACTTCCGCCAGCCAGCCGCGCGCCAGCC 83
Db 932 CTCGAAGACCGCCGACAGCGCTCTCGATATGGCCAGCGCCGCGGACGCTTCCTGGCC 991
QY 84 ACCATCTAGGTAAACAGCGACCGGGCTGTCGGAGCTGACCTCGCCCTGTGCC 138

Db 992 AACATGAGCCAGAGATCCGACGCGCTGAACGGCTGCTCGGCATGCTCTCGC 1046

RESULT 14

US-09-252-991A-9541
; Sequence 9541, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9541
; LENGTH: 2583
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9541

Query Match 23.0%; Score 31.8; DB 4; Length 2583;
Best Local Similarity 54.8%; Pred. No. 1.2;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 24 CTCGGAGAGCTCGCCGACAGCATAGTACTTCCGCCAGCCAGCCGCGCGCCAGCC 83
Db 1096 CTCGAAGACCGCCGACAGCGCTCTCGATATGGCCAGCGCCGCGGACGCTTCCTGGCC 1155
QY 84 ACCATCTAGGTAAACAGCGACCGGGCTGTCGGAGCTGACCTCGCCCTGTGCC 138
Db 1156 AACATGAGCCAGAGATCCGACGCGCTGAACGGCTGCTCGGCATGCTCTCGC 1210

RESULT 15

US-09-252-991A-14871
; Sequence 14871, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14871
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14871

Query Match 22.6%; Score 31.2; DB 4; Length 999;
Best Local Similarity 52.3%; Pred. No. 1.7;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 7 TCCGCTGGCTCTCACCCCTCGGAGAGCTGCGCCGACAGCATAGTACTTCCGCCAGCC 66
Db 493 TCGCCGACCGCGGACCGCTCTGTTCCCGGACGAAGTGCACGTTTCCCGGACGCTGGCC 552
QY 67 ACCGCCGCGCGCCAGCCAGCATGCTAGGTAAACAGCGACCGGGGCTGTCGGGACTGACCC 126
Db 553 AAGTGCTGGCCAGCAAGCTTCGAAGTCACTTTCAACCGTGACTTCCGGGCGGTGATC 612

Qy 127 TCGCCCTGTGCC 138
| | | | |
Db 613 CAGGCTTGTGCC 624

Search completed: April 26, 2004, 15:48:02
Job time : 60.5 secs


```
QY 121 TGACCCCTCGCCCTGTGCC 138
Db 121 TGACCCCTCGCCCTGTGCC 138

RESULT 5
US-10-017-273A-1
; Sequence 1, Application US/10017273A
; Publication No. US20030119714A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Naylor, Alasdair M.
; APPLICANT: Van Der Graaf, Pieter H
; APPLICANT: Wayman, Christopher P.
; TITLE OF INVENTION: Treatment of Male Sexual Dysfunction
; FILE REFERENCE: PC22013
; CURRENT APPLICATION NUMBER: US/10/017,273A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/265,358
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: GB 0030647.2
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 0108730.3
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: GB 0120679.6
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 09/905,846
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/291,722
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 09/895,367
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-017-273A-1

Query Match 98.8%; Score 136.4; DB 15; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.4e-34;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGTCCGC 60
Db 1 ACCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGTCCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCCGAC 120
Db 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTGCC 138
Db 121 TGACCCCTCGCCCTGTGCC 138

RESULT 6
US-10-191-997-94
; Sequence 94, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: NPY: Acc. No. US20030207834A1 K01911
US-10-191-997-94

Query Match 98.8%; Score 136.4; DB 16; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.4e-34;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGTCCGC 60
Db 1 ACCCATCCGCTGGCTCTACCCCTCGGAGACGCTCGCCGACGATAGTACTTGTCCGC 60
QY 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACCGGGGCTGTCCGAC 120
Db 61 CCAGCCACGCGCGCGCCAGCCACCATGCTAGTAAACAGCGACTGGGGCTGTCCGAC 120
QY 121 TGACCCCTCGCCCTGTGCC 138
Db 121 TGACCCCTCGCCCTGTGCC 138

RESULT 7
US-10-036-542-16
; Sequence 16, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002p1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (118)..(118)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (254)..(255)
```

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (839)-(839)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (887)-(887)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (897)-(897)
OTHER INFORMATION: n equals a,t,g, or c
US-10-036-542-16

Query Match 89.3%; Score 123.2; DB 15; Length 969;
Best Local Similarity 96.2%; Pred. No. 2.4e-30;
Matches 125; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 9 CGCTGGCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTCCGCCCGACAC 68
|||
Db 250 CGAGNCTCTACCCCTCGGAGAGCTCGCCGACAGCATAGTACTTCCGCCCGACAC 309
|||
Qy 69 GCCCGCGCGCAGCCACCATCTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTC 128
|||
Db 310 GCCCGCGCGCAGCCACCATCTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTC 369
|||
Qy 129 GCCCTGTCCC 138
|||
Db 370 GCCCTGTCCC 379
|||

RESULT 8

US-10-036-542-41
Sequence 41, Application US/10036542
Publication No. US20030083481A1
GENERAL INFORMATION:
APPLICANT: Birse et al.

TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1
CURRENT APPLICATION NUMBER: US/10/036,542
PCT/US00/19666
PRIORITY FILING DATE: 2002-01-07
PRIORITY FILING DATE: 2000-07-20
PRIORITY FILING DATE: 1999-07-21
PRIORITY FILING DATE: 1999-08-13
PRIORITY FILING DATE: 1999-08-17
PRIORITY FILING DATE: 1999-08-17
PRIORITY FILING DATE: 1999-10-06
PRIORITY FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 553
TYPE: DNA
ORGANISM: Homo sapiens
US-10-036-542-41

Query Match 79.3%; Score 109.4; DB 15; Length 553;
Best Local Similarity 98.4%; Pred. No. 6.9e-26;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCCCGACACGCCCGCG 75
|||
Db 1 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCCCGACACGCCCGCG 60
|||
Qy 76 GCCGAGCCACCATGTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTGCTGT 135
|||
Db 61 GCCGAGCCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGA-CCTCGCCCTGT 119
|||
Qy 136 CCC 138
|||

Db 120 CCC 122

RESULT 9

US-09-925-300-100
Sequence 100, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
PCT/US00/05988
PRIORITY FILING DATE: 2001-08-10
PRIORITY FILING DATE: 2000-03-08
PRIORITY FILING DATE: 60/124,270
PRIORITY FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 100
LENGTH: 599
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (583)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (584)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (599)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-100

Query Match 79.3%; Score 109.4; DB 9; Length 599;
Best Local Similarity 98.4%; Pred. No. 6.9e-26;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 16 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCCCGACACGCCCGCG 75
|||
Db 14 TCTCACCCTCGGAGACGCTCGCCGACAGCATAGTACTTCCGCCCGACACGCCCGCG 73
|||
Qy 76 GCCGAGCCACCATGTAGGTAAACAGCGACCGGGCTGTCCGGACTGACCCCTGCTGT 135
|||
Db 74 GCCCA-CCACCATGTAGGTAAACAGCGACTGGGGCTGTCCGGACTGACCCCTGCTGT 132
|||
Qy 136 CCC 138
|||
Db 133 CCC 135
|||

RESULT 10

US-10-036-542-42
Sequence 42, Application US/10036542
Publication No. US20030083481A1
GENERAL INFORMATION:
APPLICANT: Birse et al.

TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1
CURRENT APPLICATION NUMBER: US/10/036,542
PCT/US00/19666
PRIORITY FILING DATE: 2002-01-07
PRIORITY FILING DATE: 2000-07-20
PRIORITY FILING DATE: 1999-07-21
PRIORITY FILING DATE: 1999-08-13
PRIORITY FILING DATE: 1999-08-17
PRIORITY FILING DATE: 1999-10-04
PRIORITY FILING DATE: 1999-10-06

US-10-002-048A-3

